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2265 83.7 544 24 ABU67464 Human secreted/ 2265 83.7 544 24 ABU651110 Human PRO940 pc 2265 83.7 544 24 ABU65322 Human PRO polyr 2265 83.7 544 24 ABU58458 Human PRO polyr 2265 83.7 544 24 ABU58458 Human PRO polyr	n PRO po		ABU56989	24	544		5 8	N	15
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	secreted/	-	ABU67464	24	544		5	N	10

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secret

New human obesity protein binding protein-2 homologue nucleic acids, polynucleotides and polypeptides useful for producing medicament for

WPI; 2000-664992/64. N-PSDB; AAA37847.

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RESULT 2
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ID AAU8
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AC AAU8
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Best Local S
Matches 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       obsity and/or obsity-related disorders. The hOB-BP2h nucleic acids a useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence is a human obesity protein binding protein-2 homologue (hOB-Bp2h) of the invention. The hOB-Bp2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-Bp2h nucleic acids are
  immune
tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating
                                                        Sialic acid-binding Ig-related lectin, Siglec-BMS-L3-995-3.
                                                                                     05-JUN-2002
                                                                                                                                             AAU87087
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              sialic acid-binding Ig-related lectin; SIGLEC; asthma; system disease; leukaemia; allergy; inflammatory disea
  system damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
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                                                                                                                                                                                                                                HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                                        PLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEEL
                                                                                                                                                                                                                                                                                                                                                                                    SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                           LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAALSSQGTKFTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSESYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                 HYATLNFPGVRPRPEARMPKGTQADYAEVKFQ
                                                                                                                                                                                                                                                                       PLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEEL
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                                                                                     (first entry)
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  leukaemia;
c rhinitis;
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Pred. No. 5.1e-206;
; Mismatches 0;
    allergy; inflammatory osteoarthritis; Crohn'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders
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     natory disease;
Crohn's diseas
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FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV

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TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD

LVISISRDNTPD

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                                                                                                                                                                                                                                             CC represent potential markers for screening, diagnosis, prognosis, CC represent potential markers for screening, diagnosis, prognosis, CC drollow-up assays, and imaging methods. (I) is useful as a target for CC drollow-up assays, and imaging methods. (I) is useful as a target for CC drollow-up assays, and inflammatory diseases such as allergic rhinitis, CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, CC conjunctivitis, etc. (I) is also useful for monitoring the course of CC conjunctivitis, etc. (I) is also useful for monitoring the course of CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis CC methods, and to detect the presence and/or amount of SIGLEC-BMS creening genomic CC library to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy CC library to isolate a genomic clone of SIGLEC-BMS gene substituted with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also cused to detect, sort or isolate cells expressing SIGLEC-BMS proteins CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins cand in diagnostic imaging technology. AAU87074-AAU87089 represent CC human SIGLEC amino acid sequences of the invention.
                                                                                                                                Query Match
Best Local S
Matches 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising (I) are useful for treating immune system diseases such as asthma, leukaemia or other allergic or inflammatory diseases. Extracellular domains of (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
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510; Conserv
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                                                                          MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
FKAVTETTKGAPVATNHOSREVEMSTRGRFOLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
                                                        MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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The invention relates to an isolated SIGLEC related lectin) protein (I). Pharmaceutical
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                                                                                                                                                                                                                                                                        Sialic acid-binding
                          Claim 5; Figure 2B; 209pp; English.
                                                Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
                                                                                                           Longphre M,
                                                                                                                                            21-JUL-2000; 2000US-220139P
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                                                                                                          Chang H,
                                                                                                                                                                                                                                                                                        (first entry)
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(static acid-binding Ig-
compositions comprising
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asthma, and inflammatory diseases such as allergic rhinitis,

Conjunctivitis, crohn's disease, psoriasis, rheumatoid arthritis,

Cc conjunctivitis, etc. (I) is also useful for monitoring the course of

CC disease or disorders, and for identifying agents that bind with and/or

CC modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid

CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis

CC methods, and to detect the presence and/or amount of SIGLEC-BMS

CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample.

CC (II) are useful as nucleic acid probes are useful for screening genomic

CC ilbrary to isolate a genomic clone of SIGLEC-BMS gene copy

CC number is determined for detecting diseases or disorders associated with

CS SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS proteins

CC used to detect, sort or isolate cells expressing SIGLEC-BMS proteins

CC and in diagnostic imaging technology. AAU87074-AAU87089 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful for treating immune system diseases such as asthma, leukae or other allergic or inflammatory diseases. Extracellular domains of represent potential markers for screening, diagnosis, prognosis, follow up assays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cal Similarity
452; Conserv
NOKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                                                                      KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
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75.1%;
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Pred. No. 4.9e-172;
1; Mismatches 1;
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98US-0079294

98US-0079663

98US-0079664

98US-0079663

98US-0079786

98US-0079786

98US-0080105

98US-008015

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98US-008033

98US-008033

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98US-0078886.
98US-0078910.
98US-0078936.
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PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083559.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-008533.
PR 13-MAY-1998; 98US-008533.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085697.
PR 12-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086446.
PR 22-MAY-1998; 98US-0086486.
PR 22-MAY-1998; 98US-0086496.
PR 22-MAY-1998; 98US-008708.
PR 22-MAY-1998; 98US-0086496.
PR 22-MAY-1998; 98US-0086496.
PR 22-MAY-1998; 98US-008708.
PR 22-MAY-1998; 98US-008708.
PR 23-MAY-1998; 98US-008708.
PR 24-MAY-1998; 98US-008708.
PR 25-MAY-1998; 98US-008708.
PR 26-MAY-1998; 98US-008708.
PR 27-MAY-1998; 98US-008708.
PR 28-MAY-1998; 98US-008708.
PR 28-MAY-
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Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;

R WPI; 1999-551358/46. R N-PSDB; AAZ34109.

New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -

Claim 12; Fig 93; 530pp; English.

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAX41685 to AAX41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present invention.

Sequence 544 AA;

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Query Match

83.7%; Score 2265; DB 20; Length 544;

Best Local Similarity 74.8%; Pred. No. 5.2e-171;

Matches 450; Conservative 1; Mismatches 3; Indels 148; Gaps

Qy 1 MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW 60
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ARBSULT 5
AAB44280
IID AAB44
XX AAB4
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   08-MAR-1999;
12-MAR-1999;
29-MAR-1999;
21-APR-1999;
21-APR-1999;
14-MAR-1999;
23-JUN-1999;
23-JUN-1999;
26-JUL-1999;
29-CCT-1999;
02-DEC-1999;
02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; transmembrane protein; PRO; EST;
expressed sequence tag; detection; cancer.
                                                                                                                                                                                                                                                                 14-SEP-2000
                                                                                                                                                                                                                                  18-FEB-2000;
                                                                                                                                                                                                                                                                                                   WO200053756-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     Human PRO940 (UNQ477) protein sequence SEQ ID
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FQ 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSDESKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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 99US-01310232
99US-0131445
99US-014287
99US-0141037
99US-0145698
99US-0165506
99WO-US28513
99WO-US28551
99WO-US28555
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                                                                                                                                                                                                                                                                                                                                                                                      cytostatic;
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N-PSDB;
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30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating blological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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Goddard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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)B; AAC78510.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
GEFTCHARHPLGSOHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLELCLALIIMKILP
                                                                  NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                        FKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                               LVISISRDNTPD----
                                                                                                                                                                                                                                                                                                 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                  ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                      FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                        WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                           LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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Filvaroff E,
Godowski PJ,
Kuo SS, Nap,
Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 AA;
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99WO-US31274.
99WO-US31274.
99WO-US00219.
2000WO-US00277.
2000WO-US00376.
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74.8%;
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[A, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Botstein D, Desnoyers L, Eaton DL; Fong S, Gao W, Gerber H, Gerritsen Grimaldi CJ, Gurney AL, Hillan KJ; ier MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2265; DB 21;
Pred. No. 5.2e-171;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in detection methods, and to modulate
                                                                                                                                                          ---PPENLRVMVSQANRTVLE
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14 - MAR - 2000;
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21 - MAR - 2000;
22 - MAR - 2000;
23 - MAR - 2000;
24 - APR - 2000;
11 - APR - 2000;
12 - APR - 2000;
25 - APR - 2000;
25 - APR - 2000;
25 - APR - 2000;
27 - MAY - 2000;
28 - JUN - 2000;
29 - JUN - 2000;
20 - JUN - 2000;
21 - AUG - 2000;
22 - AUG - 2000;
23 - AUG - 2000;
24 - AUG - 2000;
24 - AUG - 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU29082 standard;
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         2000US-198121P
2000US-198585P
2000US-199397P
2000US-199550P
2000US-2015169
2000US-2015169
2000WO-US13705
2000WO-US14042
2000WO-US14941
2000WO-US15264
2000WO-US15264
2000WO-US15264
2000WO-US15264
2000WO-US15264
2000WO-US15264
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2000US-196000P.
2000US-196187P.
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2000US-192655P.

2000US-193032P.

2000US-193053P.

2000WS-193053P.

2000US-194449P.

2000US-194447P.
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2000WO-US05841.
2000US-187202P.
2000US-186968P.
2000US-189320P.
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2000WO-US06884.
2000US-190828P.
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2000US-196820P.
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Matches

450;

Conservative

1;

Mismatches

Indels 148;

Gaps

Similarity

61

FKAVTETTKGAPVATNHOSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYEFRV 120

FKAVTETTKGAPVATNHOSREVEMSTRGREOLTGDPAKGNCSLVIRDAOMODESOYFFRV ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180

120

60 60

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363 331 303 271 243 253 183 241 141 181 121 121 61

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GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP

422 390 362

NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE

330

WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE

LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP

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270

242 252 182 240

302

LVISISRDNTPD------

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. CC The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of CC expression of a PRO polypeptide in a test sample of cells from the animal CC and a control sample of normal cells, whereby a higher level of CC expression in the test sample indicates the presence of a tumour in the CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats CC and rabbits but are preferably human. The polypeptides can be used to CC stimulate tumour necrosis factor (TNF) alpha release from human blood, CC when contacted with it. A specific polypeptide can be used to stimulate tumour or differentiation of chondrocyte cells. The PRO CC proteins can be used to determine the presence of tumours and also CC susceptibility to tumour development, particularly adrenal, lung, colon, CC breast, prostate, rectal, cervical, or liver tumours, in mammalian CC subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.
     Query Match
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01-DEC-2000;
20-DEC-2000;
                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids encoding PRO polypeptides, used presence of tumours, such as prostate and breast tun to screen for modulators of the compounds -
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Score 2265; DB 22; Pred. No. 5.2e-171;
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		tic; TNF-alpha; blood; Cyte cell; proliferation;		RNOKATPNSPRTPLPPGAPSPESKK 450
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 16-SEP-1998;
07-OCT-1998;
                                 02-JUL-2002; 2002US-0188767
                                                                                US2003036156-A1
                                                                                                                           cartilage disorder;
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   The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating trelease of tumour necrosis factor alpha (TNF-alpha) from human blood contacting the blood a PRO polypeptide, a method for stimulating the
                                                                                             Claim
                                                                                                                      New secreted and transmembrane PRO polypeptides and nucleic useful in gene therapy, in chromosome and gene mapping, as c markers, in tissue typing, and in chromosome identification
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2000WO-US132678.
2000WO-US32678.
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2000WO-US319595.
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Best Local
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       08-MAY-2003
                                    ABU61110,
                                                                 ABU61110
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450; Conserv
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                                                                                                                                                                                                                                                    KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
                                                                                                                                                                                                                                                                                                                                                                                     NLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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    (first entry)
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                                                                Protein; 544
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1; Mismatches
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.2e-171;
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30-NOV-1999
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10-DEC-1999
11-DEC-1999
30-DEC-1999
30-DEC-1999
30-DEC-1999
05-JAN-2000
06-JAN-2000
06-JAN-2000
01-FEB-2000
02-MAR-2000
02-MAR-2000
01-MAR-2000
01-MAR-2000
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13 NOV-1997
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08-MAR-1999;
10-MAR-1999;
14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO940 polypeptide.
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2000WO-US00376
2000WO-US00365
2000WO-US053041
2000WO-US053041
2000WO-US05319
2000WO-US05319
2000WO-US0543705
2000WO-US13705
2000WO-US13705
2000WO-US15264
2000WO-US20710
2000WO-US20710
2000WO-US20710
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2001WO-US20710
2001WO-US20710
2001WO-US20710
2001WO-US207106
2001WO-US21066
2001WO-US21066
2001WO-US21066
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2001WO-US21066
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970S-06364P
980S-077450P
980S-077652P
980S-077649P
980S-077691P
980S-07791P
980S-078906P
980S-078910P
980S-078910P
980S-078939P
980S-078939P
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99WO-US28565.
99WO-US30095.
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99WO-US31274
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99WO-US28313
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99WO-US05190
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98US-079663P

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CC polypeptides are secreted and transmembrane proteins. The PRO cc polypeptides are secreted and transmembrane proteins. The PRO cc polypeptides are useful for detecting other PRO polypeptides, for clinking bloactive molecules to cells expressing PRO polypeptides, core for modulating biological activities of cells expressing PRO cc for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The polypeptides, and for for identifying agonists or antagonists. The cc polypeptides are useful for creating immune disorders, diabetel or antibody, and causes cc apoptosis or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, c cardiac insufficiency, nervous system disorders, kidney disorders, come and cartilage disorders or arthritis, tumours, and wound healing. The polynucleotide sequences encoding PRO polypeptides are useful as thybridisation probes, in chromosome and que mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy.

ABUG1071-ABUG1164 represent the human PRO polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara
Goddard
Kljavin
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27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
27-MAR-1998;
30-MAR-1998;
30-MAR-1998;
30-MAR-1998;
30-MAR-1999;
117-MAR-1998;
07-OCT-1998;
07-OCT-1998;
07-OCT-1998;
07-DCC-1998;
07-DCC-1998;
07-DCC-1998;
07-DCC-1999;
11-MAR-1999;
11-MAR-1999;
11-MAY-1999;
11-M
                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are neefful for detecting other PRO polypeptides, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
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DB; ABX92481.
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98US-079689P

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98US-079920P

98US-079923P

98US-0105413

98US-0105413

98US-0168973

98US-0187368

98US-026768

98US-026768

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99US-0254465

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99US-02548651

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99US-02548651

99US-03611832

99US-0380138

99US-0380138

99US-0380138

2000US-0709238

2001US-081674

2001US-0854208

2001US-0854208

2001US-0854208

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data f
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f E, Fong S, Gao W, Ger
PJ, Grimaldi JC, Gurney
Napier MA, Pan J, Paor
TA, Tumas D, Williams F
                     for this
  USPTO
web
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site
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was
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Best Local S
Matches 450
                                                                              Human; PRO; cytostatic; chromosome mapping; gene mapping;
protein electrophoresis; tumour necrosis factor-alpha; TNF-alpha; blood;
                             US2003032102-A1
                                                                                                              Human PRO polypeptide #59.
                                                                     chondrocyte differentiation;
                                                                                                                                     16-MAY-2003
                                                                                                                                                                             ABU65322
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                                                                                                                                                                             standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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                                                                                                                                    (first
                                                                                                                                                                               Protein;
                                                                                                                                    entry)
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74.88;
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Pred. No. 5.2e
1; Mismatches
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                                                                      chondrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                         proliferation; tumour
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.2e-171;
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	2002US - 0173697. 98WO - US13330. 98WO - US21108. 99WO - US25108. 99WO - US25109. 99WO - US21091. 99WO - US21091. 99WO - US21091. 99WO - US283301. 99WO - US283301. 99WO - US283301. 99WO - US28331. 99WO - US2831. 90WO - US2831. 90WO - US283.
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10-SEP-1998;
10-SEP-1998;
10-SEP-1998;
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                     Similarity
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                                                                                                                                                                                                                                                                                      LVISISRDNTPD-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                         WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                 ------PPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                    LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                                                                                                                                                                                                                                                                                                                 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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98US-09687P

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98US-091544P.
98US-091478P.
98US-091486P.
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ced. No. 5.2e-171;
Mismatches 3;
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02-JUN 1999
01-SEP-1999
15-SEP-1999
30-NOV-1999
01-DEC-1999
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02-DEC-1999
05-JAN-2000
18-FEB-2000
18-FEB-2000
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01-JUN-2001
01-JUN-2001
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07-OCT-1998;
01-DEC-1998;
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10-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P.
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99WO-USO5028
99WO-USO5028
99WO-USO5190
99WO-USO20111
99WO-US21091
99WO-US28501
99WO-US28501
99WO-US28501
99WO-US08504
2000WO-US06341
2000WO-US0504
2000WO-US05052
2001WO-US05052
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98WO-US25108
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61 61 Query Match Best Local S Matches 450

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18-SEP-1997
17-OCT-1997
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28-OCT-1997
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29-OCT-1997
29-OCT-1997
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97US-062250P

97US-062250P

97US-063140P

97US-063111P

97US-063141P

97US-063544P

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97US-0664103P

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Best Local Similarity
Matches 450; Conserv
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10-JUN-1998

10-JUN-1998

11-JUN-1998

12-JUN-1998

13-JUN-1998

14-JUN-1998

15-JUN-1998

16-JUN-1998

17-AUG-1998

18-AUG-1998

19-AUG-1998

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11-AU
   Conservative
                                                                        98US-0881738P

98US-088124P

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98US-0898175P

98US-089512P

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98US-090254P

98US-090254P

98US-090254P

98US-090254P

98US-09069P

98US-09162P

98US-09162P

98US-09163P

98US-09189

98US-09189

98US-09189

98US-09189

98US-09189

98US-09189

98US-09882P

98US-09882P
                    83.7%;
74.8%;
 Score 2265; DB 24;
Pred. No. 5.2e-171;
1; Mismatches 3;
                                   Length
     Indels 148;
                                      544;
   Gaps
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RESULT 14
ABU55994
ID ABU5
XX ABU5
AC ABU5
XX Huma
XX USON
FOR HOMC
XX USON
PN USON
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PF 20--
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10-SEP-1998;
                                                  20-JUN-2002;
                                                                                 30-JAN-2003
                                                                                                               US2003022298-A1
                                                                                                                                            Homo
                                                                                                                                                                       tumour; adrenal tumour; lung tumour; colon tumour; breast tumour;
prostate tumour; rectal tumour; cervical tumour; liver tumour;
bone disorder; cartilage disorder; arthritis; sports injury.
                                                                                                                                                                                                              Human; secreted protein; transmembrane protein; pRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell differentiation;
                                                                                                                                                                                                                                                                           Human secreted/transmembrane protein, PRO940.
                                                                                                                                                                                                                                                                                                                                                                       ABU55994 standard;
                                                                                                                                                                                                                                                                                                                                           ABU55994;
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                                                                                                                                           sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGPRPLGLELPGVKAGDSGRYTCRAENKLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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                                                   2002US-0176913
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         97WO-US20069
98WO-US18824
                                                                                                                                                                     cartilage disorder; arthritis; sports injury.
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15-SEP-1999
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08-TAN-2000
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16-SEP-1998;
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99WO-US28301
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99WO-US28564
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99WO-US30911
99WO-US30991
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99WO-US30299
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99WO-US30219
2000WO-US03565
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2000WO-US04341
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99WO-US10733.
99WO-US12252.
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99WO-US205944.
99WO-US21090.
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                                                                                            NLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
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        NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                                                                           WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                          LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
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98US-089514P.
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98US-089563P.
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74.8%;
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; Pred. No. 5.2e
1; Mismatches
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5.2e-171;
es 3;
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RESULT 15
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     99WO-US10733
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99WO-US21190
99WO-US28501
99WO-US28501
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Best Local Similarity 74.8%;
Matches 450; Conservative
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Pred. No. 5.2e-171;
1; Mismatches 3;
                                                                                                                                                                                    Length
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FQ 512 	NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK	KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 4	GETTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP :	NLGNGTSLPVLEGOSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE :	WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE	LVISISRDNTPD	TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 2	FKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120 ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
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Job time: 58 secs

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29-Aug-1997

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Gaps

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Minimum DB seq length: 0
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Gapop 10.0 , Gapext 0.
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1 MLLPLLLSSLLGGSQAMDGR...
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   GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen
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myelin-associated
myelin-associated
staloadhesin - mou
differentiation an
CD22 homolog/B lym
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m33-B isoform - mo
               hemicentin precurs myosin-light-chain
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A;Gene: GDB:CD33
A;Gross-references: GDB:119762; OMIM:159590
A;Map position: 19q13.3-19q13.4
C;Superfamily: immunoglobulin homology
C;Keywords: glycoprotein; surface antigen; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>F;1-17/Domain: extracellular #status predicted <EXT>
F;260-282/Domain: transmembrane #status predicted <CYM>
F;283-364/Domain: intracellular #status predicted <CYT>
F;180,113,160,209,230/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    myeloid cell surface antigen CD33 precursor - human C;Species: Homo sapiens (man) C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989
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A30521
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A; Residues: 1-364 <SIM>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol. 141, 2797-2800, 1988
A;Title: Isolation of a cDNA encoding CD33, a differentiation antigen of myeloid A;Reference number: A30521; MUID:89009814; PMID:3139766
A;Accession: A30521
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                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                              SWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLIS
                                                                                                                              LSAAPTSLG--PRTTHSSVLIITPRPQDHGTNLTCQVKFAGAGVTTERTIQLNVTYVPQN
                                                                                                                                                TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                     ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180
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                                                                                             LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARL
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32.8%; Pred. No. 4.3e-40;
Live 59; Mismatches 137; Indels 148;
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Result

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A;Residues: 1-626 <SPA>
A;Residues: 1-626 <SPA
A;Residues: 1-626 <A; Miyatake.
A;Residues: 1-626 <A; Miyatake.
A;Reference number: A33263; MUID:89392063; PMID:2476987
                                                                                                                                                                             myelin-associated glycoprotein precursor - human
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 31-Dec-1993 #sequence_revision 16-Aug-1996 #text_change 29-Oct-1999
(;Accession: A61084; A33263; PC2011
R;Spagnol, G.; Williams, M.; Srinivasan, J.; Golier, J.; Bauer, D.; Lebo, R.V.;
J. Neurosci. Res. 24, 137-142, 1989
A;Title: Molecular cloning of human myelin-associated glycoprotein.
A;Reference number: A61084; MUID:90064604; PMID:2479762
A;Accession: A61084
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A:Title: Molecular cloning of two isoforms A:Reference number: I52590; MUID:94250900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          m33-B isoform - mouse
C:Species: Mus sp. (mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change
C:Accession: I52590
                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                               A; Status: not compared with
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                                                                                                                                                          conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NVTRKSGQMRELVLVAVGEATVKLLILG--LCLV 261
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Pred. No. 1.1e-28;
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C. Superfamily: myelin-associated glycoprotein; immunoglobulin homology C.; Superfamily: myelin-associated glycoprotein; phosphoprotein; transmemb F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-626/Product: myelin-associated glycoprotein #status predicted <MAT>
F.35-102/Domain: immunoglobulin homology <INM>
F.118-120/Region: cell attachment (R-G-D) motif
F.514-536/Domain: transmembrane #status predicted <TMM>
F.514-536/Domain: cell attachment (R-G-D) motif
F.99,223,246,315,406,450,454/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Burger, D.; Pidoux, L.; Steck, A.J.
Biochem. Biophys. Res. Commun. 197, 457-464, 1993
A; Title: Identification of the glycosylated sequons of l
A; Reference number: PC2011; MUID:94092116; PMID:7505568
A; Accession: PC2011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A33263
A;Molecule type: mRNA
A;Residues: 1-613,'T',615-626 <SAT>
A;Cross-references: GB:M29273; NID:g187292; PIDN:AAA59545.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;573/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:120702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: MAG; GMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 84-98,'X',100-110;210-222,'X',224;245,'X',247-253;309-318,'XXX';396-405,
C; Comment: This protein is a neural cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 137
                                                                                                                                                                                 383
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137; Conserv
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                                                IAIVCYITQTRRKKNVTESPSFSAGDNPPVLFSSDFRISGAPEKYESERRLGSERRLLGL
                                                                                                                                                                                                                                                                                                                                                                                                               GYYACLAENAYGQDNRTVGLSVMYAPWKPTVNGTMVAV-EGETVSILCSTQSNPDPILTI
                                                                                                                                                                                                                             HCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNESEREFVYSERSGLVLTSILTL---
                                                                                                                                                                                                                                                                                                                       FKEKQILSTVIYESELQLELPAVSPEDDGEYWCVAENQYGQRATAFNLSVEFAPVLLLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIVEMNSSVEATEGSHVSLLCGADSNPPPLLTWMRDGTVLREAVAESLLLELEEVTPAED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEPAVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQASFPNTTLQFEGYASMDVKYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AALSS-QGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYPPVVFKSRTQVVHESFQGRSRLLGDLGLRNCTLLLSNVSPELGGKYYFRGDLGGYNQY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FWIRVQ---
                                                                                                                                                                                 LIIMKILPKRRTQTETP-----RPRFSRHSTILDY-----INVVPTAGPLA----
                                                                                                                                                                                                                                                                                                                                                                   TQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDLVISIS-----RDNTPDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFSEH----SVLDIVNTPNIVVPPEVVAGTEVEVSCMVP---DNCPELRPELSWLGHEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                        RGQAQAPPRVICTARNLYGAKSLELPFQGAHRLMWAKIGPVGAVVAFAIL
                                                                                         ·QKRNQKATPNSPRTPLPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQANRTV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 304.5; DB 1;
Pred. No. 3.5e-13;
0; Mismatches 229;
                                                                                                                                                                                                                                                                           -STAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSW
                                                                                                                                                                                                                                                                         -SNGAFL-----GIGITALLFLCLA 382
                                                                                         -GAPSP-ESKKNQKKQYQLPSF 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PENLRVMV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        626;
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419 359 359 302 300 261 180

67

23;

protein

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glycop

A; Gene: MAG		
<pre>C;Comment: The papers cited va C;Genetics:</pre>	463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNRHGTTARQLRFHHPGGLVWAK 513	당
C; Comment: The long form predo	364SNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 406	Q
A; Cross-references: GB:M11721;	403 SFNISVEYPPLVLPASRCTAGGDGVRCVCMVNSIPDSSLVFELPTRNQTVSDGHRDFTAA 462	Ъ
A; Molecule type: mRNA A: Residues: 'KS' 311-626 \PF2>	347 SLSUSVHYKKGLI	Qy
A; Accession: I52892 A:Status: preliminary: transla	VLRGGKVMAAAIYEDHVTMEMRPARPEDGGTY	рb
A; Title: Cellular localization A: Reference number: I52892; MU	287 CLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEETTCHARHPLGSQHV 346	Qy
<pre>cold Spring Harb. Symp. Quant.</pre>		Ę
A; Cross-references: GB:M36702;		? \$
A; Molecule type: mRNA	DENT DUMUSOAN PHVI FIN TONOTICS BUT EXOCS	Ş
A;Accession: I56564 A;Status: preliminary; transla		밁
A; Reference number: I56564; MU	223 GVSAORTVRLRVAYAPRDLVISISRDNTPDP 253	Qy
J. Neurosci. 5, 1781-1802, 198	164 CPPLRPLITWTGTEELLDPIGKERIEDDLGSKSLLGSLRFRPRKEDLGRRVGCGVTFINS 223	В
A; Note: the authors translated	173 CPPPSESWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRK 222	φ
	RGDLGGYNQYSF-SEHAELDVWAAPHLEVPHELVAGSEAEI	р
A; Molecule type: mRNA A; Residues: 'KS', 311-626 <sut></sut>	114 -SQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE 172	Qy
A; Reference number: A90836; MCA; Accession: A90836		, 5
A; Title: Identifying the prote		? .
R;Sutcliffe, J.G.; Milner, R.J.	63 AVTETTKGAPVATNHOSREVEMSTRGREOLTGDPAKGNCSLVIRDAOMODE- 113	Q V
A;Residues: 1-626 <sal> A;Cross-references: GB:X05301;</sal>	4 LVLTVLLMGTGCISAPWAAWMPPKMAALSGTCVQLPCRFDYPEELRPASIGGLWY- 58	DЬ
A; Molecule type: mRNA	5 LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK 62	Qy
A; Title: The anilho acto sequent A; Reference number: A27185; MC h.accostics. A27185	Matches 148; Conservative 89; Mismatches 224; Indels 199; Gaps 29;	Ma
J. Cell Biol. 104, 957-965, 15	uery Match 11.2%; Score 302.5; DB 2; Length 620;	n O
A; Cross-references: GB: M14871;	;222,314,331,405,449/Binding site: carbohydrate (Asn) (covalent) #status predicted	F; 22
A; Molecule type: mRNA A: Residues: 1-626 < ARO>	3-101/Domain: immunogiobulin homology <imw></imw>	F: 50
A; Reference number: A941/3; Mu A; Accession: A94175	;18-620/Product: Schwann cell myelin protein #status experimental <sch></sch>	F;18
le: Mol	:Keywords: glycoprotein; transmembrane protein	
R; Arquint, M.; Roder, J.; Chia Proc. Natl. Acad. Sci. U.S.A.	;Comment: This protein is expressed on all external membranes of Schwann cells. ;Superfamily: myelin-associated glycoprotein; immunoglobulin homology	C) Su
A; Cross-references: GB:M16800;	1 1	A; Re
A: Residues: 1-626 < LAT>	ccession: PS0356	A; Ac
A; Reference number: A29028; MCA; Accession: A29028	A; Note: the species of quall is not identified	A; NO
le: Two forms of 18236,	A;Cross-references: GB:SB3711; NID:g245729; PIDN:AAB21466.1; PID:g245730	A; Cr
R;Lai, C.; Brow, M.A.; Nave, F	A; Molecule type: mRNA A; Residues: 1-620 <dul></dul>	A; Mo
C;Date: 19-FeD-1984 #sequence_ C;Accession: A29028; A94175; P	593; MU1D:92153423;	A; Ac
C; Species: Rattus norvegicus (itle: Molecular characterization of the schwann cell myelin protein, SMP: structural	A; T1
myelin-associated glycoproteir N:Alternate names: 1B236: brai	R;Dulac, C.; Tropak, M.B.; Cameron-Curry, P.; Rossier, J.; Marshak, D.R.; Roder; J.; Le Neuron 8, 323-334, 1992	R; Du
RESULT 5 BNRT3	;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000 ;Accession: JH0593; PS0356	C; Da
	ss: Coturnix coturnix japonica (Japanese quail)	C;Speci
Db 574 GAMERWALGVKE		JH0593
Qy 453KKQYQLPSFPEPKS		550
Db 514 VGPVGAVVAFAIVIAV	HSDL-GKRPTKDSYTLSEELA	망
Qy 407STILDYINVVPT	462 PEPKSSTQAPESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510	Q

A; Gene: MAG

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12; NID:9203181; PIDN:AAA40831.1; PID:9203182
k.J.; Bloom, F.E.
it. Biol. 48, 477-484, 1983
on and function of the proteins encoded by brain-specific
MUID:84206577; PMID:6586369
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A27185; A90836; I56564; I52892; A03138; A26362
K.A.; Noronha, A.B.; Quarles, R.H.; Bloom, F.E.; Milner,
. 84, 4337-4341, 1387
inyelin-associated glycoprotein, a cell adhesion molecule
MUID:87232001; PMID:2438699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TY>
4; GB:J00756; NID:g56879; PIDN:CAA,24786.1; PID:g818027
E p18236
Led the codon CAG for residue 350 as Asn
L.F.; Milner, R.J.; Sutcliffe, J.G.
985
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ila, L.S.; Down, J.; Wilkinson, D.; Bayley, H.; Braun, P.,
ila, 4, 600-604, 1987
ind primary structure of myelin-associated glycoprotein.
MUID:87092455; PMID:2432614
1; NID:g206780; PIDN:AAA42082.1; PID:g206781 ains five presumably extracellular domains that are distance dominates in early postnatal life; alternative splicing transless of predict the mature protein to begin at residue
                                                                                                                                                                                                          lated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mapping of 18236, a brain-specific neuronal polypeptide of MUID:85263773; PMID:4020419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tein products of brain-specific genes with antibodies MUID:83259254; PMID:6347394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; NID:g56611; PIDN:CAA28920.1; PID:g56612.J.; Shinnick, T.M.; Bloom, F.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ences of the myelin-associated glycoproteins: homology to {\tt MUID:87166195}; {\tt PMID:2435742}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Colman,
1987

    NID:g205267; PIDN:AAA41556.1; PID:g205268
    COlman, D.R.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVVCYLSQSRRKKGAGSPEVTPVQPMAGPGGDPDLDLRPQQVRWLR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTAGPLAQKRNQKATPNSPRTPLPP-----GAPSPESKKNQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lated from GB/EMBL/DDBJ
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RESULT 6
BNRP13S
myelin-associated glycoprotein precursor, short spince
N;Alternate names: 1B236; brain neuron cytoplasmic prot
C;Species: Rattus norvegicus (Norway rat)
C;Aate: 30-Jun-1990 #sequence_revision 30-Jun-1990 #te
C;Accession: B29028; B27185; A6005
C;Accession: B29028; B27185; A6005
R;Lai, C.; Brow, M.A.; Nave, K.A.; Noronha, A.B.; Qua-
R;Lai, C.; Brow, Sci. U.S.A. 84, 4337-4341, 1987
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C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology
C;Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; trans
F;1-19/Domain: signal sequence #status predicted <STG>
F;0-626/Product: myelin-associated glycoprotein, long splice form #status predicted <MP
F;35-102/Domain: immunoglobulin homology <IMM1>
F;118-120/Region: cell attachment (R-G-D) motif
F;152-219/Domain: immunoglobulin homology <IMM3>
F;254-307/Domain: immunoglobulin homology <IMM3>
F;340-394/Domain: immunoglobulin homology <IMM5>
F;340-394/Domain: immunoglobulin homology <IM5-
F;340-394/Domain: immunoglobulin homology <IM5-
F;340-394/Doma
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.537-626/Domain: intracellular #status predicted <INT>
.99,223,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSNGAFLGIGITALLFLCLALI------IMKILPKRR-TQTETPRP-RFSRHSTILDYI 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAV-EGETVSILCSTQSNPDPILTI
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Pred. No. 1.4e-12;
5; Mismatches 239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -PEPKSSTQAPESQESQE
                                                          Quarles,
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                                                       R.H.; Bloom, F.E.;
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Best Local
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mes 110; Conserv
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                                                          FKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP-----
                                                                                                   TQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLISTA
                                                                                                                                                      GIYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAV-EGETVSILCSTQSNPDPILTI
                                                                                                                                                                                                                                              VIVEMNSSVEATEGSHVSLLCGADSNPPPLLTWMRDGMVLREAVAESLYLDLEEVTPAED
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GEPTVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP

--MVSQANRTV------LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSW 302

SQGT-----KPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP

RDLVISIS--

--RDNTPDP

-PENLRY-

300 259 240 238 180 186

TFSEH-----SVLDIINTPNIVVPPEVVAGTEVEVSCMVP----DNCPELRPELSWLGHEGL NFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTGAALS NYPPVVFKSRTQVVHESFQGRSRLLGDLGLRNCTLLLSTLSPELGGKYYFRGDLGGYNQY KGAPVATNHQSREVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRY FWIMISASRGGHWGAWMPSSISAFEGTCVSIPCRFDFP~-DELRPAVVHGVWYFNSPYPK FWIRVO-----ESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTETT

128

Conservative

64;

Pred. No. 3.3e-12; 4; Mismatches 185;

Indels

115;

Gaps

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C;Superfamily: myelin-associated glycoprotein; immunoglobulin homology C:Keywords: alternative splicing; brain; cell adhesion; duplication; glycoprotein; F;1-19/Domain: signal sequence #status predicted <SIG> F;20-582/Product: myelin-associated glycoprotein, short splice form #status predict F;35-102/Domain: immunoglobulin homology <IMM1> F;118-120/Region: cell attachment (R-G-D) motif F;118-120/Region: cell attachment (R-G-D) motif F;152-219/Domain: immunoglobulin homology <IMM2> F;254-307/Domain: immunoglobulin homology <IMM3> F;254-307/Domain: immunoglobulin homology <IMM3> F;254-307/Domain: immunoglobulin homology <IMM3> F;254-307/Domain: immunoglobulin homology <IMM3>
                                                                                                                       F;425-490/Domain:
F;514-536/Domain:
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A; Residues: 419-582 <SAL>
A; Cross references: GB:X06554; NID:g56614; F
A; Cross references: GB:X06554; NID:g56614; F
Brain Res. Mol. Brain Res. 4, 143-155, 1988
A; Title: Differential splicing of MAG trans(
A; Reference number: A60055
A; Accession: A60055
                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Comment: The sequence contains five C:Comment: The short form is found in C:Genetics:
                                                                                                                                                                           F;340-394/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 565-582 <TRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: A27185; MUID:87166195; PMID:2435742 A;Accession: B27185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession. The type: mRNA
A; Molecule type: mRNA
A; Residues: 1-582 < LAI>
A; Cross-references: GB:M22357; NID:g205271;
A; Cross-references: GB:M22357; Colman, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion molecule A;Reference number: A29028; MUID:87232001; PMID:2438699
A;Accession: B29028
                                                           ,246,315,332,406,450,454/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holmes, W.P.; Co. 34, 957-965, 1987
                                                                                           transmembrane #status predicted intracellular #status predicted
                                                                                                                                               immunoglobulin homology <IMM4>
10.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of MAG transcripts during
Score 289.5;
Pred. No. 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       presumably the adult;
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Roder, J.C.
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                       DB 1;
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                    Length
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myelin-associated glycoprotein - mouse
C;Specles: Mus musculus (house mouse)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 23-Jul-1999
C;Accession: B3785; A33785; S05687; S02374
R;Fujita, N.; Sato, S.; Kurihara, T.; Kuwano, R.; Sakimura, K.; Inuzuka, T.; Takahashi, Biochem. Blophys. Res. Commun. 165, 1162-1169, 1989
A;Title: cDNA cloning of mouse myelin-associated glycoprotein: a novel alternative splic A;Recession: B33785; MUID:90121220; pMID:2482022
A;Accession: B33785
A;Accession: B37785
A;Accession: B37785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Superfamily: myelin-associated glycoprotein; immunoglobulin C:Keywords: alternative splicing; glycoprotein; transmembrane F:152-219/Domain: immunoglobulin homology <IMM2>
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A; Molecule type: mRNA
A; Residues: 310-374;566-582 <FU4>
A; Cross-references: EMBL:X07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 310-374;566-573,584-588
A;Cross-references: EMBL:X07849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Developmentally regulated alternative splicing of brain myelin-associated A;Reference number: S02374; MUID:88242820; PMID:2454205 A;Accession: S05887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M31811; NID:g199016; PIDN:AAA39487.1; PID:g199017 R;FUJ1ta, N.; Sato, S.; Kurihara, T.; Inuzuka, T.; Takahashi, Y.; Miyata FEBS Lett. 232, 323-327, 1988
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A; Residues: 1-582 <FU3>
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A; Residues: 1-637 <FUJ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FWIRVQES -------VMVPEGLCISVPCSFSYPRODWTGSTPAYGYWFKAVTETT
                                                                                                                                                                                                                                                                                                                                 TFSEH----SVLDIVNTPNIVVPPEVVAGTEVEVSCMVP---DNCPELRPELSWLGHEGL
                                                                                                                                                                                                                                                                                                                                                                          NEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP--PSFSWTGAALS 186
LTIFKEKQILATVIYESQLQLELPAVTPEDDGEYWCVAENQYGQRATAFNLSVEFAP---
                                     LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI 359
                                                                                GVYACLAEN - - - AYGQDNRTVELSVMYAPWKPTVNGTVVAV - EGETVSILCSTQSNPDPI
                                                                                                                                                               VIVEMNSSVEAIEGSHVSLLCGADSNPPPLLTWMRDGMVLREAVAKSLYLDLEEVTPGED
                                                                                                                                                                                                           RDLVISIS------RDNTPDP-----
                                                                                                                                                                                                                                                GEPTVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQAAFPNTTLQFEGYASLDVKYPP
                                                                                                                                                                                                                                                                                       SQGT-----KPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FWIMISASRGGHWGAWMPSTISAFEGTCVSIPCRFDFP--DELRPAVVHGVWYFNSPYPK
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                                                                                                                      --PENLRYMYSQANRTY-----LENLGNGTSLPVLEGQSLCLVCVTHSSPPAR
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Pred. No. 4.4e-12;
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I49583
                                                                                                                 J. Immunol. 151, 175-187, 1993
A;Title: Organization of the murine Cd22 locus. Mapping A;Reference number: 149583; MUID:93315834; PMID:8100843
A;Accession: 149583
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                           differentiation antigen - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
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S50065
                                                                          A; Molecule type: mRNA
A; Residues: 1-862 < RES>
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A;Molecule type: mRNA
A;Residues: 1-1694 <CRO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Crocker, P.R.; Mucklow, EMBO J. 13, 4490-4503, 19
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C;Species: Mus musculus (house mouse)
C;Date: 07-May_1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: S50065
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                                                      A;Cross-references: GB:L16928; NID:g348965; PIDN:AAA02562.1;
                                                                                                                                                                                                                          R; Law, C.
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25.7%;
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; Pred. No. 1.4e-08;
52; Mismatches 179;
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PMID:7925291
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character

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RESULT 10
A46512
CD22 homolog/B lymphocyte-restricted adhesion molecule - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995
C;Accession: A46512
R;Torres, R.M.; Law, C.L.; Santos-Argumedo, L.; Kirkham, P.A.; Grabstein, K.; Parkhouse, J. Immunol. 149, 2641-2649, 1992
A;Title: Identification and characterization of the murine homologue of CD22, a B lymphod A;Reference number: A46512; MUID:93017867; PMID:1401903
A;Accession: A46512; MUID:93017867; PMID:1401903
A;Accession: A46512
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-868 <TOR>
A;Experimental source: B cell lymphoma 38C13
A;Note: sequence extracted from NCBI backbone (NCBIP:116156)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFN-------WAF
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NVYTESKLTFQPKWTDHGKSVKCQVQHSSK-VLSECTVHLDVKYTPKLEIKVNPTEVEKN
                                   SHF--SVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP---
                                                                                                                                                                                                                                               EGLCISVPCSFS--YPRQDWTGSTPAYGYWFKAVTETTKG----APVATNHQSREVEMS 85
                                                                      PYIQMPSEIRESQSVTLTCGLNFSCFGYDILLKWFLEDSEITSITSSVTSITSSVTSSIK 212
                                                                                                       PDVYIPETLEPGOPVTVICVFN------WAFEECPPPSFSWTGAALSSQGTKPTT 194
                                                                                                                                          KQGRVTFLGNRI-DNCTLKIHPIRANDSGNLGLRMTAGT----ERWMEPIHLNVSEKPFQ
                                                                                                                                                                           TRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQK 145
                                                                                                                                                                                                              EGACIRIPCKYKTPLPKARLDNILLFQNYEFDKATKKFTGTCLYNATKTEKDPESELYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGSQHV--SLSLSVHYKKGLISTAFSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQSLCLVCVTHSSPPA-RLSWTQRGQVLSPSQPSD-PGVLELPRVQVEHEGEFTCHARHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGT----ERWMEPIHLNVSEKPFQPYIQMPSEIRESQSVTLTCGLNFSCFEYDILLQWFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDSKITSVTPSVTSITSSVTSSIKNVYTESKLTFQPKWTDHGKSVKCQVQHSSE-VLSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLILGHAASAQYSSANDWTVDHPQTLFAWEGACIRIPCKYKTPLPKARLDNILLFQNYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLSSLLGGSQAMDGRFW-IRVQESVMVPEGLCISVPCSFS--YPRQDWTGSTPAYGYWF
                                                                                                                                                                                                                                                                                           Conservative
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21.7%; Pred. No. 2.8
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                                                                                                                                                                                                                                                                                    Pred. No. 2.8e7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 227; DB 2
Pred. No. 1e-07;
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2.8e-07;
hes 173; Indels 101
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A;Cross-references: GDB:127545; OMIM:107266
A;Map position: 19q13.1-19q13.1
C;Superfamily: immunoglobulin homology
C;Reywords: alternative splicing; B-cell; cell adhesion;
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-510/Domain: extracellular #status predicted <EXT>F;432-484/Domain: immunoglobulin homology <IMM>F;511-529/Domain: transmembrane #status predicted <TMM>F;530-647/Domain: intracellular #status predicted <CYT>F;67,101,112,135,164,231,268,302,397,457/Binding site: ce
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A;Title: The B-cell antigen A;Reference number: A35648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B-cell adhesion protein CD22 alpha splice form precursor - human C;Species: Homo sapiens (man) C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: GDB: CD22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:x52785; NID:g29778; PIDN:CAA36988.1;
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A; Residues: 1-647 < STA>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                             1 MLLPLLLSSLLGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFS------YPRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
           WEEPSLGVLKIQNVGWDNTTIACAACNSWCSWASPVALNVQYAPRDVRVRKIKPLSEIHS
                                                                                                                                               SCYGYPIQLQWLLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQWSHHGKI-VTCQLQDA
                                                                                                                                                                                                                   HLNDSGQLGLRMES----KTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNF 165
                                                                                                                                                                                                                                                      QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFN- 167
                                                                                                                                                                                                                                                                                         EYNKNTSKFD--GTRLYESTKDGKVP-----SEQKRVQFLGDKNK-NCTLSIHPV
                                                                                                                                                                                                                                                                                                                         DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108
                                                                                                                                                                                                                                                                                                                                                            LLGPWLLLLVLEYLAFSDSSKWVFEHPETLYAWEGACVWIPCTYRALDGDLESFILFHNP
                                                                               DGKFLSNDTVQLNVKHPPKKVTTVIQNPMPIREGDTVTLSCNYNSSNPSVTRYEWKPHGA
                                                                                                                                                                                      ------WAFEECPPPSFSWTGAALSSQGT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSVTMTCRVNSSNPKLRTVAVSWFKDGRPLEDQELE-QEQQMSKLILHSVTKDMRGKYRC
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19.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 206.5; DB 2;
Pred. No. 1.8e-06;
7; Mismatches 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monocyte and pmID:1691828
                                              SAQRTVRLRVAYAPRDL - - - -
                                                                                                                                                                                    -----KPTTSHFSVLSFTPRPQDH
                                                                                                                  -TDLTCHVDFSRKGV-----
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>>>:	Qy 1 MLLPLLLSSLLGGSQAMDGRFWI-RVQESVMVPEGLCISVPCSFSYPRQ 48	
> > <u>&</u> 7 1	Query Match 7.5%; Score 202.5; DB 2; Length 847; Best Local Similarity 21.0%; Pred. No. 4.7e-06; Matches 98; Conservative 69; Mismatches 182; Indels 117; Gaps 19;	
>>>>>>	F;30-847/Product: B lymphocyte cell adhesion protein *status predicted <mat> F;346-398/Domain: immunoglobulin homology <imm1> F;609-661/Domain: immunoglobulin homology <imm2> F;609-661/Domain: immunoglobulin homology <imm2> F;688-706/Domain: transmembrane *status predicted <tra> F;67,101,112,135,164,231,363,445,448,479,574,634/Binding site: carbohydrate (Asn) (coval F;764,789/Binding site: phosphate (Thr) (covalent) *status predicted</tra></imm2></imm2></imm1></mat>	
PPPPP	A;Cross-references: GDB:127545; OMIM:107266 A;Map position: 19q13.1-19q13.1 A;Introns: 138/1; 240/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3 A;Introns: 138/1; 140/1; 329/1; 417/1; 503/1; 591/1; 679/1; 711/2; 804/3 C;Superfamily: immunoglobulin homology C;Keywords: alternative splicing; B-cell; cell adhesion; dimer; glycoprotein; phosphoprof; Keywords: signal sequence #status predicted <sig></sig>	
₩₽₽₽ ₽	A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 121-269,'T',271-473,'K',475-614,'R',616-638,'Y',640-711,777-847 <wil2> A;Cross-references: GB:S61375; NID:g385980; PIDN:AAC18956.1; PID:g3184492 C;Genetics: C;Genetics:</wil2>	
0 D D D	A;Title: Genomic structure and chromosomal mapping of the human CD22 gene. A;Reference number: I56171; MUID:93267103; PMID:8496602 A:Accession: T66171	
×	A; Cross-references: GB:X59350; NID:g36090; PIDN:CAAA2006.1; PID:g36091 A; Cross-references: GB:X59350; NID:g36090; PIDN:CAAA2006.1; PID:g36091 A; Experimental source: B lymphocyte A; Note: the authors translated the codon AAT for residue 358 as Met A; Note: the authors translated the codon AAT for residue 358 as Met A; Nulson, G.L.; Najfeld, V.; Kozlow, E.; Menniger, J.; Ward, D.; Kehrl, J.H.	
OOOZZ	J. Exp. Med. 173, 137-146, 1991 A;TILLe: CDNA cloning of the B cell membrane protein CD22: a mediator of B-B cell intera A;Reference number: JH0371; MUID:91086838; PMID:1985119 A;Accession: JH0371 A;Molecule type: mRNA	
ਲ ਕ ਹ	C;Date: 30:Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-2000 C;Date: 30:Sep-1991 #sequence_revision 30-Sep-1991 #text_change 31-Jan-2000 C;Accession: JH0371; I56171 R;Wilson, G.L.; Fox, C.H.; Fauci, A.S.; Kehrl, J.H.	
D '6	RESULT 12 JH0371 B-cell adhesion protein CD22 beta splice form precursor - human N;Alternate names: B-cell membrane protein CD22 C:Species: Homo sapiens (man)	
ם פֿ ם	Qy 485 LNFPGVRPRPEARMPKGTQADYAEVK 510 	_
2 0 1	Qy 425 KRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYAT 484 :	
5 'Ö 'E	Qy 371 IGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQ 424 : :: :: : : : :: : :: :	_
2 <i>9</i> 1	Qy 312 SQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLG 370	
E 9	Qy 273 GNGTSLPVL	
2 0	Qy 242VISISRDNTPDPPENLRVMVSQANRTVLENL 272	

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                                                                                                                                                                                                                                                    166
                               334 TCHARHPLGS--QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALL 377
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SCVAENILGTGQRGPGAELDVQYPPKKVTTVIQNPMPIREGDTVTL 440
                                                                                                                                                                                         QDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSN----PEYTTV 277
                                                                                                                                                                                                                                                                                                                                              QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFN- 167
                                                                                                                                                                                                                                                                                                                                                                               EYNKNTSKFD--GTRLYESTKDGKVP-----
                                                                                                                                                                                                                                                                                                                                                                                                            DWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDA 108
                                                              ILHSPAVEGSQVEFLCMSLANPLPTNYTWYHNGKEM --
                                                                                                                            SWLKDGTSLKKQNTFTLNLREVTKDQSGKYCCQVSNDVGPGRSEEVFLQVQYAPEPSTVQ
                                                                                                                                                          ------NLR-VMVSQANR---TVLENLGNGTS---------
                                                                                                                                                                                                                                                                                                                 HLNDSGQLGLRMES----KTEKWMERIHLNVSERPFPPHIQLPPEIQESQEVTLTCLLNF
                                                                                                                                                                                                                     -DFSRKGVS-----AQRTVRLRVAYAPRDLVI------SISRDNTPDPPE----
                                                                                                                                                                                                                                                    SCYGYPIQLQWLLEGVPMRQAAVTSTSL----TIKSVFTRSELKFSPQWSHHGKIVTCQL 221
                                                                                           ---LPVLEGQSLCLVCVTHSSP-PARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEF 333
                                                                                                                                                                                                                                                                                   -WAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV 217
                                                                                                                                                                                                                                                                                                                                                                               -SEQKRVQFLGDKNK-NCTLSIHPV 109
                                                              -QGRTEEKVHIPKILPWHAGTY 394
                                                                                                                            337
                                                                                                                                                          277
                                                                                                                                                                                                                      255
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: A32164; A30127; B30127; A48078; S45664; S65939; A30847; G44476 R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft Proc. Natl. Acad. Sci. U.S.A. 86, 1668, 1989 A;Reference number: A32164
A;Contents: erratum A32164
biliary glycoprotein 1 precursor, splice form a - human
biliary glycoprotein 1 precursor, splice form a - human
N;Alternate names: transmembrane carcinoembryonic antigen 1 (TM1-CEA); transmembrane
N;Contains: biliary glycoprotein 1, splice form b; biliary glycoprotein 1, splice for
C;Species: Homo sapiens (man) A; Molecule type: 1;Accession: A32164 13 1-526 <HIN> mRNA

A;Cross-references: GB:J03858; NID:g179439; PIDN:AAA51826.1; PID:g179440
R;Hinoda, Y.; Neumaier, M.; Hefta, S.A.; Drzeniek, Z.; Wagener, C.; Shively, L.; Heft Proc. Natl. Acad. Sci. U.S.A. 85, 6959-6963, 1988
A;Title: Molecular cloning of a cDNA coding biliary glycoprotein I: Primary structure A;Reference number: A94206; MUID:88320555; PMID:2457922 ጓ;Residues:

A;Contents: annotation A;Note: the sequence shown in this reference has been completely corrected in referen A;Note: T.R.; Kretschmer, A.; Austen, D.A.; Goebel, S.J.; Hart, J.T.; Elting, J.J. A;Title: Carcinoembryonic antigens: alternative splicing accounts for the multiple mRA;Reference number: A92752; MUID:89139550; PMID:2537311
A;Accession: A30127 R;Barnett, T.R.; Kretschmer, A.; J. Cell Biol. 108, 267-276, 1989

A; Molecule type: mRNA A; Residues: 1-526 <BARl> A; Cross-references: EMBL A; Accession: A; Experimental source: splice B30127 EMBL: X16354; NID: g37197; PIDN: CAA34404.1; PID: g37198; EMBL: X14784 form

A; Molecule type: mRNA A; Residues: 1-319, LD, 417-526 <BAR2> A; Cross-references: EMBL:X14831; NID:937199; A; Experimental source: splice form b R; Barnett, T.R.; Drake, L.; Pickle II, W. Mol. Cell. Biol. 13, 1273-1282, 1993 PIDN:CAA32940.1; PID:g37200; EMBL: X14784

A;Reference number: A48078; MUID:93140
A;Accession: A48078
A;Molecule type: mRNA
A;Residues: 124-141,'H',417-526 <BAR3> A;Title: Human biliary glycoprotein gene: characterization of a family of novel alter A;Reference number: A48078; MUID:93140765; PMID:8423792

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F;252-301/Domain: immunoglobulin homology <IMM2>
F;351-391/Domain: immunoglobulin homology <IMM3>
F;341-398/Domain: immunoglobulin homology <IMM3>
F;457-454/Domain: transmembrane #status predicted <IMM>
F;457-454/Domain: intracellular #status predicted <IMT>
F;453-526/Domain: intracellular #status predicted <INT>
F;104,111,115,152,182,197,208,224,232,254,274,288,292,302,309,345,351,363,378,405,475/Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-terming (C;Keywords: alternative splicing; glycoprotein; surface antigen; transmembrane protein F;1-34/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN> F;1-34/Domain: signal sequence *status predicted <SIG> F;35-526/Product: biliary glycoprotein 1, splice form a *status predicted <MATA> F;55-428/Domain: extracellular *status predicted <EXT> F;55-319, 'D, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predicted <P;55-141, 'H, '417-526/Product: biliary glycoprotein 1, splice form b *status predi
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C; Superfamily: carcinoembryonic antigen; car
C; Keywords: alternative splicing.
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
A;Note: only a part of the coding sequence is given
R;Khan, W.N.; Fraeengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S.
Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembrane communication communicatio
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A;Cross-references: EMBL:X67277; NID:g29447; PIDN:CAA47694.1; R;Nedellec, P.; Turbide, C.; Beauchemin, N.
Eur. J. Blochem. 231, 104-114, 1995
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A; Residues: 1-21 <NED>
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A;Note: neither the complete nucleic acid sequence nor the complete translation are R;Hauck, W.; Nedellec, P.; Turbide, C.; Stanners, C.P.; Barnett, T.R.; Beauchemin, N Eur. J. Biochem. 223, 529-541, 1994
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Best Local S
Matches 130
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A;Experimental source: splice form x
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                                                                                                                                                                                                                                                                                                                                                                                        114
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                     ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR
                                                                                                                                                           VRLRVAYAPRDL-VISISRDNTPDPPENLRVMVSQANRT--VLENLGNGTSLPVLE----
                                                                                                                                                                                                                                                                                                                                                                                                                                       MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                             FEECPPPSFSWTGAALSSOGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                                                                                                                                                                                                                                                                                                                                             QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYSWYKG - - ERVDG -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY 57
                                                                                          -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ-----LF
                                                                                                                                                                                                                                   ---ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT 113
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Pred. No. 3
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.5e-05;
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A;Introns: 18/1; 53/3; 118/1; 139/3; 169/1; 229/1;
C;Superfamily: advanced glycosylation end products
C;Keywords: receptor; transmembrane protein
F;31-100/Domain: immunoglobulin homology <IMM>
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C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T09062
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LGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQ
                                                                                                                                                                                                                                                                           QANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLEL
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                                                                                                                                                PRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY--
                                                                                                                                                                                                                            PEGGI--
                                                                                                                                                                                                                                                                                                                                                TVIPTQGGTHPTFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQPVTV-ICVFNWAFEECPPPSFSW--TGAALSSQGTK-----PTTSHFSVLS-F
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                                                                    PEVGHEDEGTYSCVATHPSHGPQESPPVSIRVTETGDEGPAEGSVGESGLGTLALALGIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEVKFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL:AF030001; NID:g2564945; PID:g2564950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, Library, October 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the mouse major histocompatibility locus class III region
                                                                                                                                                                                                              -VAPGGTVTLTCAISAQPPPQVHWIKDGAPL-PLAPSP--VLLL
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NGAFLGIGITALLFLCLA 382
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                                                                                                                                         ---KKGLISTAFSNGAF
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368 286 322 241 262 191 202

156

homology

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A:Tille: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD protein adhesion molecules, and epidermal growth factor.

A:Reference number: A41736; MUID:92112994; PMID:1730768

A:Accession: S19256

A:MOLecule type: mRNA

A:Residues: 1-57, 'D', '59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R'

71-2979, 'H', '2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3

A:Cross-references: EMBL:X62515

R:Trygyason, K.

Submitted to the EMBL Data Library, October 1991

A:Reference number: 57-7946

A:Roccession: S77946

A:Roccession: S77946

A:Roccession: 57-7946

A:Roccession: 57-7946

A:Roccession: 57-7946

A:Roccession: 57-7946

A:Roccession: S7946

A:Roccession: A40306; MUID: 9120660; PMID:1685141

A:Roccession: A41059

A:Roccession: A40306; MUID: 9120660; PMID:1685141

A:Roccession: A40306; MUID:91365376; PMID:1685141

A:Roccession: A40306; MUID:91365376; PMID:1679749

A:Roccession: A40306; MUID:91365376; PMID:1679749

A:Roccession: A40306; MUID:91365376; PMID:1679749
A; Reference number: A33625; MUID:90078352; PMID:26
A; Accession: B33625
A; Molecule type: protein
A; Residues: 1379-1384, 'X', 1386-1388, 'X', 1390-1398
A; Accession: A33625
A; Molecule type: protein
A; Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Decies: Homo sapiens (man)
C:Dete: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Nov-199
C:Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A4173
C:Accession: A38096; C.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.
J. Biol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from tor, laminin, neural cell adhesion molecules, and epidermal growth factor. A;Reference number: A38096; MUID:92235084; PMID:1569102
A;Accession: A38096; MUID:92235084; PMID:1569102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
A38096
A38096
perlecan precursor - human
perlecan precursor - human
sylvan precursor - human
perlecan precursor - human
sylvan precursor - human
sylvan sylvan precursor perlecan sulfate proteoglycan; heparan sulfate
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Species: homo sapiens (man)
c;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
                                                                                                                                                                                                                 R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulss
J. Cell Biol. 109, 3199-3211, 1989
A;Title: Matrix-associated heparan sulfate proteoglycan:
                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1018-1405', G', 1407-1409, 'G', 1411-1465 < DODS
A; Cross-references: GB: M64283; NID: g184424; PIDN: AAA52699.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kallunki, P.; Tryggvason, K.
J. Cell Biol. 116, 559-571, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-4391 <MUR>
A; Cross-references: GB: M85289; NID: g184426;
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                                                                                                                                                                                                                                                                            B.; Paulsson,
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M.; Cassiman,
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                                                                                                                                                                                                                       protein-specific
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F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;1153-1610/Domain: laminin-type EGF-like homology <EGG7>
F;1631-1668/Domain: laminin-type EGF-like homology <LEG8>
F;1677-3686/Domain: IV <DOM4>
F;1677-3686/Domain: IV <DOM5>
F;2007-2034/Domain: V <DOM5>
F;3687-4391/Domain: V <DOM5>
F;3687-3891/Domain: EGF homology <EGF1>
F;3886-3891/Domain: EGF homology <EGF>
F;3886-3921/Domain: EGF homology <EGF>
F;3953-4106/Domain: Laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
F;4147-4175/Domain: EGF homology <EGF2>
F;4149-4151/Region: motor neuron attachment (L-R-E) motif
F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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A;Cross-references: GDB:126372; OMIM:142461
A;Cross-references: GDB:126372; OMIM:142461
A;Map position: Ip36.1-1p36.1
C;Superfamily: LDL receptor ligand-binding repeat homology;
C;Keywords: chondroitin sulfate proteoglycan; glycoprotein;
F;1-21/Domain: signal sequence #status predicted <SIG>
F;1-21/Domain: merlecan #status predicted <MAT>
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F;285-319/Domain: LDL recepton
F;325-359/Domain: LDL recepton
F;368-403/Domain: LDL recepton
F;531-1676/Domain: III CDOM3>
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F;22-193/Domain: I <DOM1>
F;194-530/Domain: II <DOM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSLPGR---ATARNELLHFERAAPEDSGRYRCRV--TNKVGSAEAFAQLLVQGPPGSLPAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SISRDNTPDPPENLRYMVSQANRTVLENLGNGTSLPVLE - - - - GQSLCLVCVTHSSPPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNDGFFLKVTAL--TQKPD--VYIPE--TLEPGQPVTVICVFNWAFEECPPPSFSWTGAA
LPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR--
                                                                                      GGVVRIAHVELADAGQYRCTATNAAGTTQSHVLLLVQALPQISMPQEVRVPAGSAAVFPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYKKGLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL-VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSPAGHAEATIILHVESPPYATTVPEHASVQAGETVQLQCLAHGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCSATGSPAPTIHWSKLRSPLPWQHRLEGDTLIIPRVAQ-QDSGQYI
                                                                                                                                                                                                                                                                INIRTSVQTVVVG-HAVEFECLAL---
                                                                                                                                                                                                                                                                                                                                                      STAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFS----
                                                                                                                                                                                                                                                                                                                                                                                                                                    LRWFKEGGQLPPGHSVQDGVLRIQNLDQSCQGTYICQAHGPWGKAQASAQLVIQALPSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CVSA----GEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ
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                                                                                                                                                                         -LAQKRNQKATPNSPRTP---
                                                                                                                                                                                                                                                                -GDPKPQVTWSKVGGHLRPGIVQS
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MLLPLLLSSLLGGS
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CRACE_MOUSE
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Q97187 homo sapien
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0.0324200	SEQUENCE FROM TISSUS-Dendri MEDLINE-21359 Li N. Zhang "Cloning and binding membe J. Biol. Chem [4] SEQUENCE FROM AND 5), MUTAG MEDLINE-22152 Kitzig F., Ma "Cloning of t interaction b Biochem. Biop [5]	SEQUENCE FROM N.A SEQUENCE FROM N.A SEQUENCE G.M., Ordon Molecular charac siglec-like gene Biochem. Biophys. [2] SEQUENCE FROM N.A TISUE-Spleen; MEDLINE-21181584; Munday J., Kerr S Floyd H., Mattei j. "Identification, "Identification, siglec-lo, a nove Biochem. J. 355:4	HUMA 7; C 7; C 8-20 B-20 C ac C ac C ac C ac Taxi	153.5 151.5 147.5 142.5 141.5 141.5 140.5 139.5 139.5 139.5
334-69 1; 8257; L. F. ., Col ., Zeel ., Jord ., Mar		∞ ⊢0 x · · · ←1 σ ·	AAN STANDARD; Q96G54; Q96LC8; 2003 (Rel. 41, Creal) 2003 (Rel. 42, Last) 2004 (Rel. 42, Last) 2006 (Rel. 42, Last) 2006 (Rel. 42, Last) 2007 (Rel. 42, Last) 2008 (Rel. 42, Last) 2008 (Rel. 42, Last) 2008 (Rel. 43, Last) 2008 (Rel. 41, Last) 2009 (Rel. 42, Last)	55555555555555555555555555555555555555
7; PubMed=17; PubMed=17; Peingold Collins F.S. Zeeberg B., Prdan H., Marusina K.	. (ISOFORM cell; PubMed=113 Wan T. Zhancter1zation the Ig sup 6:28106-28 . (ISOFORM IS OF TYR-6:28106-121 PubMed=121 PubM	A. (ISOFORMS 1 AND Pubmed-11409878; Pubmed-11409878; Con M.H., Fousias ucterization, tissue (SLG2) with three Res Commun. 284 A. (ISOFORM 1). ; Pubmed-11284738; Pubmed-11284738; N.I., Cornish MG., Moore P., Characterization. el human sialic ac 489-497(2001).	DARD; LC8; 1, Cre 1, Las 2, Las 2, Las 1g·li 1g·li Chord	416 1241 1906 702 417 739 428 428 419 404 349
124 d E. .S., . B MOO R., B	DRM 2) 11358 Zhang Zhang Ation (super super -28112 DRM 3) DRM 3) LCCana LCCana Ce var Ce-10	Add-11405 a. Fouss ation, t b) with t Commun SOFORM 1) GOFORM 1) GOFORM 1) GOFORM 1) GOFORM 1) GOFORM 1) GOFORM 1)	eted t se t se t an ke 1 ke 1	
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e L.H., Derge J.(, Shenmen C.M., , Schaefer C.F., x S.I. Wang J., x Rubin G.M., I	en T., Yu Y., Wa ec-10, a novel s from human dend NATIVE SPLICING NTERACTION WITH OPEZ-BOTEL M., S f Siglec-10 and -1."; 5-362(2002).	Diamandis E.P.; plice variants."; 00-910(2001). L.; Zhang J.Q.; u D., Crocker P.I. d leucocyte expre	697 AA. update) ion update) 10 precursor (Sigl 10 the state; Vertebrata; E	TT'S
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r G.D., N.K., F., etz T.E.,	Cao x.; cid cid sid cid ws 4 of the	of a novel G.,	(Siglec-	bos taurus homo sapien gallus gall homo sapien homo sapien mus musculu homo sapien mus musculu

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT "Generation and initial analysis of more than 15,000 full-length
RT "Generation and sequences.";
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDMA sequences.";
RT "Generation binding to cells. Preferentially binds to alpha2,3- or
CC -1- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC 2,6-linked sialic acid. The sialic acid recognition site may be
CC masked by cis interactions with sialic acids on the same cell
CC upon ligand induced tyrosine phosphorylation by recruiting
CC cupon ligand induced tyrosine phosphorylation by recruiting
CC cytoplasmic phosphatase(s) via their SH2 domain(s) that block
CC signal transduction through dephosphorylation of signaling
                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                             L; AY029277; AAK40255.1; -...

L; AY029277; AAK40256.1; -...

L; AF310233; AAK55139.1; -...

L; AF311905; AAK92542.1; -...

L; AY032685; AAK51124.1; -...

L; BC009955; AAH09955.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (eosinophils, monocytes and a natural killer cell subpopulation). Isoform 5 is found to be the most abundant isoform. Found in lymph node, lung, ovary and appendix. Isoform 1 is found at high levels and isoform 2 at lower levels in bone marrow, spleen and spinal chord. Isoform 2 is also found in brain. Isoform 4 is specifically found in natural killer cells.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Tyrosine-phosphorylated.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=Short, Sv1;
IsoId=Q96LC7-2; Sequence=VSP_002565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Interacts with PTPN6/SHP-1 upon SUBCELULAR LOCATION: Type I membrane prosecreted (isoform 5).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative_splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ame=3; Synonyms=Sv3;
IsoId=Q96LC7-3; Sequence=VSP_002564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ime=1; Synonyms=Long;
IsoId=Q96LC7-1; Sequ
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SMART; SM00409; IG; 4.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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    121
                  121
                                  61
                                                                                                         Similarity
ERGSYVRYNEMNDGEFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
      ERGSYVRYNFMNDGFFLKVTALTOKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                               FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                       MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                        FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQVFFRV
                                                               MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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226
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697 AA;
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73.0%;
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Ig_c2.
Ig_MHC
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
ITH MOTIF 1.
ITH MOTIF 1.
ITH MOTIF 2.
BY SIMILARITY.
                                                                                               Score 2576.5; DB 1
Pred. No. 1.8e-173;
1; Mismatches 2;
                                                                                                                                        RAL ->
P -> S
L -> P
R -> K
                                                                                                                                                                               Y->F: ABOLISHES BINDING
S -> P (IN REF. 4).
G -> R (IN REF. 4).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                      Missing (in isoform 4).
/FTIG-VSP_002561.
TALTQKPDVYIPETLEBGQPVTVICVFNWAFEECPPDSFSW
                                                                                                                                                                                                                Missing (in isoform 2).
/FTId=VSP_002565.
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                                                                                                                                 6CB231CE49411D1B
                                                                                                                                        > P (IN REF. 4).
> R (IN REF. 4).
> A (IN REF. 1).
> A (IN REF. 3).
> S (IN REF. 3).
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RESULT 2
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Sialic acid binding Ig-like lectin 11 precursor (Siglec-11) (Sialic acid-binding lectin 11).
                                                                                                                                                       SEQUENCE FROM N.A., AND INTERACTION WITH PTPN6 AND MEDLINE-22086217; PubMed-11986327; Angata T., Kerr S.C., Greaves D.R., Varki N.M., Cro
                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
NCBI_TaxID=9606;
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Q96RL6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 607157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF337818; AAK72907.1; -.
            181
                             122
                                              121
                                                                62
                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:15622; SIGLEC11.
                                                                                                   N
                                                                                                                                               Similarity
 TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                      ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                         FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                  ERGSRVRHSFLSNAFFLKVTALTKKPDVYIPETLEPGQPVTVICVFNWAFKKCPAPSFSW
                                                                FKGRTSPKTGAPVATNNQSREVEMSTRDRFQLTGDPGKGSCSLVIRDAQREDEAWYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR007110;
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                                                                                                                                      Conservative
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                                                                                                                                                                                  74544 MW;
                                                                                                                                               55.9%;
46.6%;
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Cell adhesion; Lectin; Transmembrane; Signal; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: Phosphorylated on tyrosine residues. SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       including Kupffer cells. Also found in brain microglia. DOMAN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This is involved in downmodulation of cellular functions as the termination of the immune response.
                                                                                                              IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
ITIM MOTIF
BY SIMILARITY.
BY SIMILARIT
Score 1513.5; DB Pred. No. 7.4e-99; 1; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
SIALIC ACID BINDING IG-LIK
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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120 61

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SEQUENCE FROM N.A. (ISOFORM 3).

MEDILINE-20314554; PubMed=10856141;

Kikly K.K., Bochner B.S., Freeman S.D., Tan K.B., Gallagher K.D./Alessio K.J., Holmes S.D., Abrahamson J.A., Erickson-Miller Murdock P.R., Tachimoto H., Schleimer R.P., White J.R.;

"Identification of SAF-2, a novel siglec expressed on eosinoph mast cells, and basophils.";

J. Allergy Clin. Immunol. 105:1093-1100(2000).
                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM TISSUE=Eosinophil; MEDLINE=20092847; PubMed=100Floyd H., Ni J., Cornish A.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).
SEDLINE-20549027; PubMed-11095983;
Foussias G., Yousef G.M., Diamandis E.P.;
"Molecular characterization of a siglec8 variant containing cytoplasmic tyrosine-based motifs, and mapping of the siglec8 of the siglec8 of the siglec8. Res. Commun. 278:775-781(2000).
                                                                                                      "Siglec-8. A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILB_HUMAN STANDARD; PRT; 499 AA Q9NYZ4; Q9NYZ4; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update sialic acid binding Ig-like lectin 8 precur (Sialoadhesin family member-2) (SAF-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -ELHYASLSFQGLRLWEPADQEAPSTTEYSEIK 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLGPISQGHQHECSAGSSQDHPPPGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
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Catarrhini; Hominidae;
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DOMAIN
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Pfam; PF00047; 19; 2.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 2.
Cell adhesion; Lectin; Transm
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EMBL; AF223403;
EMBL; AF195092;
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-I DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This mot is involved in downmodulation of cellular functions as the termination of the immune response.
-I SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BLUDING IG-LIKE LECTIN) SUBFAMILY.
-I SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF310234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:10877; SIGLEC8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9NYZ4-3; Sequence=VSP_002560;
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F:transmembrane receptor P:signal transduction;
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SLAM-LIKE MOTIF.

BY SIMILARITY.

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Homo sapiens

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Best Local :
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15 FEP-2003 (Rel. 42, Last annotation update)
51alic acid binding Ig-like lectin-like 1 precursor
11ke molecule 1) (Siglec-L1).
SIGLECLI OR SLG.
                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
  "Cloning and molecular characterization of two spinew putative member of the Siglec-3-like subgroup Biochem. Biophys. Res. Commun. 284:887-899(2001).
                                 TISSUE-Bone marrow;
MEDLINE-21303046; PubMed-11409877;
Foussias G., Taylor S.M., Yousef G
Diamandis E.P.;
                                                                                                                                                                                                                   SILL_HUMAN
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Pred. No. 2.
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TTTSTVBLDVSY -> D (in isoform 2).
/FTIG-VSp_002559.
GPLTESWKDGNPLKKPPPAVAPSSGEEGELHYATLSFHKVK
PQDPQGGEATDSEYSELKIHKRETAETQACLERHNPSSKEV
RG -> VSDVGFSTPSIQPGHL (in isoform 3).
                                                                           LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RG -> VSDVGFSTPSIQPGHL (in isoform /FTId=VSP_002560. 086EFF989B74123C CRC64;
                                                                                                           Craniata; V
Catarrhini;
                                                                                                                                                                                                                   PRT;
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i; Hominidae;
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                                                                                                                                                                                                   Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein; Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
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Ig_MHC.
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SIAM-LIKE MOTIF.
SIAM-LIKE MOTIF.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC
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IG-LIKE V-TYPE 1.
IG-LIKE V-TYPE 2.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.

(GLCNAC.

(POTENTIAL).

CYTOPLASMIC (POTENTIAL)

POTENTIAL.

EXTRACELLULAR (POTENTIAL)

SIALIC ACID BINDING IG-LIKE LECTIN-LIKE

POTENTIAL.

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Name=Dony, Synonyms=Sud:
Name=Short; Synonyms=SuG-S;
IsoId=O96PO1-1; Sequence=Displayed;
IsoId=O96PO1-1; Sequence=VSP_002566;
IsoId=O96PO1-2; Sequence=VSP_002566;
InsoId=O96PO1-2; Sequence=VSP_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2] SEQUENCE FROM N.A. (ISOFORM LONG).
                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       surface.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Putative adhesion molecule that mediates dependent binding to cells. The sialic acid recognibe masked by cis interactions with sialic acids on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named Name=Long; Synonyms=SLG-L;
                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     isoforms=2;
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RESULT SILL_PANTR
ID SILL_PA
AC Q95LHO
DT 28-FEB
DT 15-SEP
DE Sialic
DE like m
GN SIGLEC
OS Pan tr.
OC Eukary
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Best Local
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                                                                                      SILL_PANTR STANDARD; PRT; 597 AA. (095LH0; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 5:alic acid binding Ig-like lectin-like 1 preclike molecule 1) (Siglec-L1).
 SEQUENCE FROM N.A MEDLINE=21523976;
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
                                                                                                                                                                                                                                                                                                                                         SNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVV---PTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                   GYEYSEINIP 594
                                                                                                                                                                                                                                                                                                 PLAQKRNQKATPNSPRTPLPP--GAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQE
                                                                                                                                                                                                                                                                                                                                                                                        QVLSPSQPSDPGYLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK---KGLISTAF
                                                                                                                                                                                                                                                            ELHYATLNFP
                                                                                                                                                                                                                                                                             PLI----ESPADDSPPHHAPPALATPSPE-----EGEIQYASLSFHKARPQYPQEQEA-I
                                                                                                                                                                                                                                                                                                                                 TLGAFGGAGATALVFLYFCIIFVVV---
                                                                                                                                                                                                                                                                                                                                                                         LTLSPSQSSNLGVLELPRVHVKDEGEFTCRAQNPLGSQHISLSLSLQNEYTGKMRPISGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S--LDPTITRSSMLSLIPQPQDHGTSLTCQVTLPGAGVTMTRAVRLNISY------
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                                                                                                                                                                                                                                                                                                                                                                                                                         ----PPQNLTMTVFQGDGTASTTLRNGSALSVLEGQSLHLVCAVDSNPPARLSWTWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                          RDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRG
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                                                               Metazoa;
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PubMed=11546777;
                                               Chordata;
Primates;
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                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 909; DB 1; 1
Pred. No. 1.7e-56;
5; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
LILLLEPILCGRVGAKEOKOVILTMOKSYUTVOGGLCVSVLC
SFSYPONGWTASDPVHGYWFRAGDHVSRNIPVATNNPARAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (in isoform Short).
/FTId=VSP_002566.
P -> T (in dbSNP:20:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEETRORFHLLGDPQNKDCTLSIRDTRESDAGTYVFCVERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_014259.
D05662176274C5C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in dbsNP:2034891).
                                                                                                                                                                                                                                                                                                                          -RSCRKKSARPAVGVGDTGMEDANAVRGSASOG
                                                                                                       precursor (Siglec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 595;
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                                                        Euteleostomi;
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Best Local S
Matches 212
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM0408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 3.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *Angata T., Varki N.M., Varki A.;

"A second uniquely human mutation affecting sialic acid biology.";

J. Biol. Chem. 276:40282-40287(2001).

-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. The sialic acid recognition site mase masked by cis interactions with sialic acids on the same cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [mmunoglobulin
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DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This is involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNGLOBULIN SUBERAMILY. SIGL. (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
             127
                                                        199
                                                                                                                                        139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface.
SUBCELLULAR LOCATION:
DOMAIN: Contains an in
                                                                                              67
                                                                                                                                                                                                                           212;
                                                                                                                                                                                   7
                                                                                                                                                                                                                                             Similarity
                                                                                                                           LSSLLGGSOAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE 66
RYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALS
                                          IPCDIPVATNTPSGKVQEDTQGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQVERGSR-
                                                                   TTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVTRDAQMQDESQYFFRVERGSYV
                                                                                                                                                                                                                       Conservative
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504 504

505 144

145 271

147 271

148 271

149 271

149 271

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140 271

141 233

344 448

144 8

144 8

142 181

142 181

142 181

143 232

144 333

344 448

448 448

149 233

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349 233

369 387 MW;
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domain;
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597
                                                                                                                                                                                                                                             33.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat.
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                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 7.

IG-LIKE 7.

I
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Pred. No. 1.7e
70; Mismatches
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                                                                                                                                                                                                                                                                                                       74C13CFA9CDB5BA5
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                                                                                                                                                                                                                                      DB 1;
.7e-56;
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                                                                                                                                                                                                                    164;
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                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                        Length 597;
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                  66;
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  186
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RESULT 6

SILS_MOUSE

ID SIRS_SOURCE

ID SIRSER-2003 (Rel. 41, Careated)

ID SIRSER-2003 (Rel. 42, Last sequence update)

ID SIRSER-2003 (Rel. 41, Last sequence update)

ID SIRSER-2003 (Rel. 42, Last sequence update)

ID SIRSER-2003 (Rel. 42, Last sequence update)

ID SIRSER-2003 (Rel. 42, Last sequence update)

ID SIRSER-2003 (Rel. 41, Last sequence update)

ID SIRSER-2003 (Rel. 42, Last sequence update)

ID SIRSER-2003 (Rel. 41, Last sequence update)

ID SIRSER-200
                                                                          SEQUENCE FROM N.A., PHOSPHORYLATION, MUTAGENESIS OF TYR-432 AND TYR-455, AND INTERACTION WITH PTPN6 AND PTPN11.

MEDLINE=21092875; PubMed=11171044;

Yu Z., Maoui M., Wu L., Banville D., Shen S.H.;

"mSiglec-E, a novel mouse CD33-related siglec (sialic acid-binding immunoglobulin-like lectin) that recruits Src homology 2 (SH2)-domain-containing protein tyrosine phosphatases SHP-1 and CRACE.
   molecules.
SUBUNIT: Homodimer; disulfide-linked. Interacts with PTPN6/SHP-1
and PTPN11/SHP-2 upon phosphorylation.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK---KGLISTAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYASLSFHKARP----QYPQEQEAIGYEYSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS
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                      EMBL; AF317298; AAG38598.1; -.
EMBL; AF339269; AAK49917.1; -.
MGD; MGI:1932475; Siglec5.
GO; GO:0004872; F:receptor activity; II
GO; GO:0005057; F:receptor signaling pa
GO; GO:0007155; P:cell adhesion; IDA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003098; Ig_C2.
InterPro; IPR003006; Ig_MHC.
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SMART; SM00408; IGc2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tities requires a license agreement (See http://www.isb-sib-send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

(SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

SIMILARITY: Contains 1 immunoglobulin-like V-type domains.

SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif binds to the SH2 domain of PTPN6/SHP-1 and PTPN11/SHP-2.
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DOMAIN: Contains an intracytoplasmic
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BY SIMILARITY.
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IG-LIKE C2-TYPE
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D-> E
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BINDING

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Query Match Best Local

Similarity

32.3%;

Score 873; DB 1; Pred. No. 4.2e-54;

Length 467;

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                                                             MEDLINE=20357333; PubMed=10801862; Zhang J.Q., Nicoll G., Jones C., Crocke "Siglec-9, a novel sialic acid binding superfamily expressed broadly on human J. Biol. Chem. 275:22121-22126(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SII9_HUMAN STANDARD; PRT; 463 AA. 099Y336; 09BYI9; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 51alic acid-binding Ig-like lectin 9 precursor
TISSUE=Peripheral
                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                           Genomics
                                                                                                                                                                                                                                                     "Toussias G., Yousef G.M., Diamandis E.P.,
"Identification and molecular characterization
the siglec family (SIGLEC9).";
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                    MEDLINE=20366134; PubMed=10903842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPVHGFWYREGTDRRKDSIVATNNPIRKAVKETRNRFFLLGDPWRNDCSLNIREIRKKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE
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                      AND MUTAGENESIS OF
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                                                                                                                                    Crocker P.R.;
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                                                                                      member of the immunoglobulin blood leukocytes."
                   ARG-120
                                                                                 leukocytes.";
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Burkhart-Schultz K., Gordon L. Dias J., Raminez M., Stilwagen S.,
A Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,
A Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
A Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J.,
A Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
A Arellano A., Sanders C., Ow D., Nolan M., Trong S., Krommiller B.,
A Arellano A.S., Carrano A.V.,
The Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
C i-- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3- or 2,6-linked sialic acid. The sialic acid recognition site may be analysis of interactions with sialic acids on the same cell
                                               GO; GO:0007166; P:cell surface InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig. InterPro; IPR003599; Ig. MHC. Pfam; PF00047; Ig; 3. SMART; SM00409; IG; 2. PROSITE; PS50835; IG_LIKE; 3. PROSITE; PS50835; IG_LIKE; 3.
Cell adhesion; Lectin; Antigen; Transmembrane; Immunoglobulin domain; Repeat; Polymorphism. SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                        EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (neutrophils and monocytes but not eosinophils). Found in liver, fetal liver, bone marrow, placenta, spleen and in lower levels in skeletel muscle, fetal brain, stomach, lung, thymus, prostate, brain, mammary, adrenal gland, colon, trachea, cerebellum, testis, small intestine and spinal cordon.

1. DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response.

2. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.

3. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

3. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>'</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Lamerdin J.E., McC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               new member of the CD33-related group of co-evolution with sialic acid synthesis J. Biol. Chem. 275:22127-22135(2000).
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Amemiya C., Yajima Y., Yazaki M.;
"Molecular cloning of a novel gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angata T., Varki A.; "Cloning, characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20357334;
                                                                                                                                                              ; GO:0005887;
; GO:0005530;
; GO:0007166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SURFACE.
SUBCELLULAR IOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed by peripheral blood
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                                                                                                                                                                                                                                                       AF247180;
AF227924;
AB026265;
AC011473;
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                                                                                                                                                                                                                                      HGNC:10878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r cloning of a novel gene, FOAP-9, wh LDL in human macrophages."; (APR-1999) to the EMBL/GenBank/DDBJ
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AAF87223.1;
AAF71455.1;
BAB41100.1;
AAG23261.1;
                                                                                                                                                              F:lectin; NAS.
P:cell surface
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                                                                                                                                                                                                 C:integral
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Y., Turitani K., Naitou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and phylogenetic analysis of siglec-9, ted group of siglecs. Evidence for id synthesis pathways.";
                                                                                                                                                                                               plasma
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., Dias J., Ramirez M., Stil
                                                                                                                                                              receptor linked
                                                                                                                                                                                               membrane;
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                               Glycoprotein;
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  SQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510 : | | | | : | : | : | : | : | : |
                                                                                                                                                                                     RLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEETCHARHPLGSQHVSLSLSVHYKKGL
                                                                                                                                                                                                                                                                                                                                                                      VISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVC---VTHSSPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLSLSWRGLTLCPSQPSNPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLQSK---
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTSVSP--LDPSTTRSSVLTLIPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDL
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                                                                       SASQGPLTEPWAEDS------PPDQPPPASAR
                                                                                                                                                             ATSGVTQGVVGGAGATALVFLSFCVIFVVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KGS-IKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWI
                                                                                                                -PTAGPLAOKRNOKATPNSPRTPLPPGAPSPESKKNOKKOYOLPSFPEPKSSTOAPESOE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 2.

ITH MOTIF.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
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; 807BDCE0D18191F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_014255
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N-LINKED
N-LINKED
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Pred. No. 6.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A -> E (in dbSNP:2258983)
/FTId=VAR_014257.
A -> D (in dbSNP:273688).
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RESULT 8

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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin 6 precursor
binding protein 1) (OB-BP1) (CD33 antigen-like
SIGLEC6 OR CD33L OR CD33L1 OR OBBP1.
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patel N., Brinkman-Van der Linden E.C Balasubramanian S., Timans J.C., Pete Varki A., Kastelein R.A.;
J. Biol. Chem. 274:28058-28058(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "OB-BP1/Siglec-6. A leptin- and sialic immunoglobulin superfamily.";
J. Biol. Chem. 274:22729-22738(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patel N., Brinkman-Van der Linden
Balasubramanian S., Timans J.C., I
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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"Molecular cloning of a novel gene similar to myeloid antigen CD33 an
its specific expression in placenta.";
Cytogenet. Cell Genet. 78:295-300(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 1 AND
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                                                                                                                                                                            TISSUE SPECIFICITY: Expressed at high levels in placenta and syncytictrophoblastic cells) and at lower levels in speripheral blood leukocytes (predominantly B-cells) and sintestine.

DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (TINM). This involved in downmodulation of cellular functions as the termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Putative adhesion molecule that mediates similc acid dependent binding to cells. Binds to alpha2,6-linked similc acid. The similc acid recognition site may be masked by cis interactions with similc acids on the same cell surface.

SUBCULT: Interacts with LEP.
SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
SECTIONARY OF STATEMENT OF 
                                                                                        (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named iso Name=1; Synonyms=Membrane-bound, CD33 IsoId=043699-1; Sequence=Displayed; Name=2; Synonyms=Secreted, CD33L2; IsoId=043699-2; Sequence=VSP_002553 Note=Should not be confused with SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted (isoform 2).
ALTERNATIVE PRODUCTS:
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be confused with SIGLEC5 which has been called
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D., Bell M.P., Bazan J.F.,
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InterPro; IPR003598; Ig_c2.
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FRL-KSKWMKYGYTSSKLSVRVMALTHRPNISIPGTLESGHPSNLTCSVPWVCEQGTPPI
               FRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPS
                                 WF-----LEGADVPVATNDPDEEVQEETRGRFHLLWDPRRKNCSLSIRDARRRDNAAYF
                                          WFKAVTETTKGA--PVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYF
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TS -> HL (IN REF. 2)
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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LS -> IY (IN REF.
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L -> F (in dbSNP:
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Q9Y286; Q9NZQ1; Q9U286; Q9U387; Q9Y502;
28 FEB-2003 (Rel. 41, Created)
28 FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin 7 precursor (Simembrane protein) (Adhesion inhibitory recptor mo.)
(p75) (D-siglec).
SIGLECT OR AIRMI.
Angata T., Varki A.;
"Siglec-7: a sialic a
superfamily.";
Glycobiology 10:431-4
                                                                                                                                                                                 Zhang W., Wan T., Cao X.;
"Characterization of a novel
Submitted (AUG-1999) to the 1
                                                                                                                                                                                                                                                                                                                              Falco M., Biassoni R., Bottino C., Vitale M., Sivori S., Augugliaro R., Moretta L., Moretta A.; "Identification and molecular cloning of p75/AIRM1, a not the sialoadhesin family that functions as an inhibitory human natural killer cells."; J. Exp. Med. 190:793-802(1999).
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Mattel M.-G., Crocker P.R.,
"Identification and characterization
expressed by human natural killer cel
J. Biol. Chem. 274:34089-34095(1999)
                                                                                                    MEDLINE=20230158; PubMed=10764831;
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             TISSUE=Dendritic cell;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lymphoid;
MEDLINE=99429884; PubMed=10499918;
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Homo sapiens (Human).

Finkarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license agreement (See http://www.isborsend an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Ito A., Handa K., Withers D.A., Satoh M., Hakomori S.;
"Binding specificity of siglec7 to disialogangliosides of renal cell carcinoma: possible role of disialogangliosides in tumor
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FEBS Lett. '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Tyrosine-phosphorylated.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CAUTION: Ref. 3 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note-No experimental confirmation available;
TISSUE SPECIFICITY: Predominantly expressed by resting and activated natural killer cells and at lower levels by grant and monocytes. High expression found in placenta, liver, list, and peripheral blood leukocytes.

DOMAIN: Contains an intracytoplasmic motif referred as monocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Interacts with PTPN6/SHP-1 upon phosphorylation SUBCELLULAR LOCATION: Type I membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disialyl GalNAc lactotetraoslylceramide). The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. Mediates inhibition of natural killer cells cytotoxicity. May play a role in hemopolesis. Inhibits differentiation of CD34+ cell precursors towards myelomonocytic cell lineage and proliferation of leukemic myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoreceptor tyrosine-based inhibitor motif (ITIM). T
is involved in downmodulation of cellular functions as
termination of the immune response. The phosphorylated
binds to the SH2 domain of PTPN6/SHP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAUTION: Ref.3 sequence differs from that shown frameshift in position 406.
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    AF170485;
AJ007395;
AJ130710;
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IsoId=09Y286-2; Sequence=VSP_002555;
ame=3; Synonyms=AIRM-3;
IsoId=09Y286-3; Sequence=VSP_002556, VSP_002558;
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ime=1; Synonyms=AIRM-1b;
IsoId=Q9Y286-1; Sequence=Displayed;
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AAF12759.1; -. CAB46011.1; -. CAB51126.1; -.
                                                                                                                                                                                                               (See http://www.isb-sib.
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SEQUENCE
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SITE
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; Cell adhesion; Lectin; Tra
                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                     VARSPLIC
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SMART; SM00408; IGc2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0004872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005887;
                     180
                                                         121
                                                                            116
  236
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AJ130712;
                                                                                             61 VHGYMFRAGNDISWKAPVATNNPAWAVQEETRDRFHLLGDPQTKNCTLSIRDARMSDAGR
                                                                                                                                                                                  Similarity
YAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS
                                                                        YFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP
                                                                                                        AYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQ
                                                                                                                                                     LLPLLLSSLLGGSQAMDGR-----FWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTP
                    PMISWMGTSVSP--LHPSTTRSSVLTLIPQPQHHGTSLTCQVTLPGAGVTTNRTIQLNVS
                                                                                                                                    MLLLLLPLLWGRERVEGQKSNRKDYSLTMQSSVTVQEGMCVHVRCSFSYPVDSQTDSDP
                                     PSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVA
                                                         YFFRMEKGN-IKWNYKYDQLSVNVTALTHRPNILIPGTLESGCFQNLTCSVPWACEQGTP
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467 1
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; CAB51128.1;
; CAB51129.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lectin; Transmembrane; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:integral to plasma membrane; TAS F:lectin; TAS.
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AAF06790.1;
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51142
                                                                                                                                                                                 30.8%; Score 832.5; DB 37.9%; Pred. No. 2.9e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
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                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity; TAS
                                                                                                                                                                                                                                                                                                                                              IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
ITIM MOTIF.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
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V -> A (IN REF.
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GTSVSPLHPSTTRSSVLTLIPQPQHHGTSLTCQVTLPGAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. SIALIC ACID BINDING IG-LIKE LECTIN 7.
                                                                                                                                                                                                                                                                                                 TTNRTIQLNVSY -> D (in
                                                                                                                                                                                                                                          Missing (in isoform 3
                                                                                                                                                                                                                                                    /FTId-VSP_002557
                                                                                                                                                                                                                                                                      /FTId=VSP_002556
                                                                                                                                                                                                                                                                                        /FTId=VSP_002555
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IG-LIKE V-TYPE
                                                                                                                                                                                                                                                           -> G (in isoform 4).
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                                                                                                                                                                                                              8AFE44462B001F52 CRC64;
                                                                                                                                                                         Mismatches
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Andreise T., Trankheim M., Attix C., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
                                                                                                                                                                                                                                                                                                                          Balasubramanian S., Timans
Varki A., Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Erythroleukemia;
MEDLINE=99557812; pubMed=10428856;
Patel N. Brinkman-Van der Linden E.C.M.,
Balasubramanian S., Timans J.C., Peterson
Varki A., Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cornish A.L., Freeman S., Forbes G., Ni J., Zhang M., Cepeda M., Gentz R., Augustus M., Carter K.C., Crocker P.R.;
"Characterization of siglec-5, a novel glycoprotein expressed on myeloid cells related to CD33.";
Blood 92:2123-2132(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Stalic acid binding Ig-like lectin 5 precursor (Siglec-5) (Obesity-binding protein 2) (OB binding protein-2) (OB-BP2) (CD33 antigen-like 2) (CD170 antigen).
SIGLEC5 OR OBBP2 OR CD33L2.
                                                                                                                                                                                                                                                                                                                                                                                                                       'OB-BP1/Siglec-6. A leptin-and sialic immunoglobulin superfamily.";
J. Biol. Chem. 274:22729-22738(1999).
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Eukaryota; Metazoa; C
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MEDLINE-98402360; PubMed-9731071;
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                                                                                                                                                                                                                                                                                                       274:28058-28058(1999).
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Primates;
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J.C., P
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Peterson
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D., Bell M.P., Bazan
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D., Bell M.P.,
                                   mediates sialic-acid
                alpha2,3-linked
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Pfam; PF00047; ig; 3.
SMART; SM00408; IGC2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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InterPro; IPR003598;
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DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). T is involved in downmodulation of cellular functions as termination of the immune response.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY. SIMILARITY: Contains 3 immunoglobulin-like V-type domai SIMILARITY: Contains 3 immunoglobulin-like C2-type domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Surface.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed by monocytic/myeloid lineage cells.
Found at high levels in peripheral blood leukocytes, spleen, bone marrow and at lower levels in lymph node, lung, appendix, placenta, pancreas and thymus. Expressed by monocytes and neutrophils but absent from leukemic cell lines representing earl
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Ig_c2.
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                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

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    /FTId=VAR_014251.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
ITIM MOTIF.
SLAM-LIKE MOTIF.
                                                                                                         /FTId=VAR_014250
F -> S (in dbSNP)
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M -> V (in dbSNP:1807124).
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Simmons D., Seed B.;
"Isolation of a cDNA encoding CD33,
myeloid progenitor cells.";
J. Immunol. 141:2797-2800(1988).
[2]
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                 Oda;
Homo sapiens (Human).
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                                                                                                                                                                   TISSUE-Promonocytic lymphoma; MEDLINE-89009814; PubMed-3139766;
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Catarrhini; Hominidae
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RA KLausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Hopkins R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquelano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.;
Prior. Natl. Acad. Sci. U.S.A. 98:5764-5769(2001).

-!- FUNCTION: Putative adhasion molecule of myelomonocytic-derived cells that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,6-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface. In the immune response, may act as an inhibitory receptor upon ligand induced tyrosine phosphorylation by recruiting cytoplasmic phosphatase(s) via their SH2 domain(s) that block signal transduction through dephosphorylation of signaling molecules. Induces apoptosis in acute myeloid leukemia (in vitro).

SUBUNIT: Interacts with prpns / orr
                                                                                                                                                                                                                                                                                    Vitale C., Romagnani C., Puccetti A., Olive D., Costello R., Chiossone L., Pitto A., Bacigalupo A., Moretta L., Mingari M.C.; "Surface expression and function of p75/AIRM-1 or CD33 in acute myeloid leukemias: engagement of CD33 induces apoptosis of leukem
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Yousef G.M., Ordon M.H., Foussias G., Diamandis E.P.;
"Genomic organization of the siglec gene locus on chromosome 19q13.4
and cloning of two new siglec pseudogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTPN11, AND MUTAGENESIS OF TYR-340
MEDLINE=99223460; PubMed=10206955;
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               <u>:</u>
                                                                                                                                                                                                                                                                    cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Freeman S.D., Kelm S., Barber E.K., "Characterization of CD33 as a new of cellular interaction molecules." Blood 85:2005-2012(1995).
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MEDLINE-22388257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10556798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed-12477932;
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                                                                                                                                                                                                                                                                                    induces apoptosis of leukemic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION
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A MIM; 159590; -.

& GO; GO:0005887; C:integral to plasma membrane; TAS.

& GO; GO:0004872; F:receptor activity; TAS.

& GO; GO:0007267; P:cell-cell signaling; TAS.

& GO; GO:0007267; P:cell-cell signaling; TAS.

& GO; GO:0007165; P:signal transduction of cell proliferation; TAS.

R GO; GO:0007165; P:signal transduction; TAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003599; Ig.

R InterPro; IPR003006; Ig_MHC.

R Pfam; PF00047; Ig; 2.

R Pfam; PF00047; Ig; 2.

R SMART; SM00409; IG; 2.

R PROSITE; PS50835; IG_LIKE; 2.

R PROSITE; PS50835; IG_LIKE; 2.
     Query
                               MUTAGEN
CONFLICT
SEQUENCE
                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                     DISULFID
DISULFID
DISULFID
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylation.

-! SUBCELLULAR LOCATION: Type I membrane protein.
-! TISSUE SPECIFICITY: Monocytic/myelold lineage cells.
-! DOMAIN: Contains two copies of an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (TIIM). This motif is involved in downmodulation of cellular functions as the termination of the immune response. The phosphorylated ITIM motif binds to the SH2 domain of prpN6/SHP-1 and/or PTPN11/SHP-2.
-! SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
-! SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
-! DATABASE: NAME-PROW; NOTE-CD guide CD33 entry; WMW="http://www.ncbi.nlm.nih.gov/prow/cd/cd33.htm".
                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content endified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sortendent.it.institutions as its content entities requires a license agreement (See http://www.isb-sortendent.it.institutions).
                                                                                                                                                                                                                                                                                                                                                   TRANSMEN
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EMBL; BC028152; AAH28152.1;
PIR; A30521; A30521.
HSSP; Q62230; 1QFO.
                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
       Match
                                                                                                                                                                                                                                                                                                                                                                                         adhesion; Lectin; Antigen; Transmembrane; Signal; Glycoprotein; phorylation; Immunoglobulin domain; Repeat; Multigene family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262230; 1QFO.
HGNC:1659; CD33.
                                             358
69
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    25.6%;
                              MW;
                                                                                                                                                                                                                                        POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE.

ITIM MOTIF 1.

ITIM MOTIF 2.

BY SIMILARITY.

BY SIMILARITY.
                                                                                          N-LINKED (GLCNAC...) (P

Y->A: ABOLISHES BINDING T
                                                                    PTPN11;
CELLS.
  Score 694;
                                         Y->A, F: REDUCES BINDING G -> R (IN REF. 2).
                                                                                                                                                                                                      PHOSPHORYLATION (INVOLVED IN PTPN6 AND PTPN11).
                                                                                                                                                                               PTPN6
                                                                                                                                                                                          PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
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                           1973E196940FB16F
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Length 364;
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RESULT 12
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gene clusters. 76:45128-45136(2001).

J. Biol. Chem. 276:45128-45136(2001).

-!- FUNCTION: Putative adhesion molecule that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,3-linked sialic acid. The sialic acid recognition site may be masked by cis interactions with sialic acids on the same cell surface.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Predominantly expressed by immature monocytic/myeloid lineage cells in bone marrow. Also found at lower levels in mature neutrophils and monocytes.

-!- DOMAIN: Contains an intracytoplasmic motif referred as immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular functions as the
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Angata T., Hingorani R., Varki N.M., Varki A.;
**Cloning and characterization of a novel mouse Siglec, mSiglec-F:
**Cloning and characterization of the mouse and human (CD33) Siglec-3-related
                                                                                                                                                                                                           gene clusters."
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sialic acid binding Ig-like lectin-F precurso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SILF_MOUSE
0920G3;
                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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Rodentia;
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Sciurognathi; Muridae; Murinae; Mus
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9; Mismatches 137;
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InterPro; IPR003598; Ig_c
InterPro; IPR003006; Ig_m
InterPro; IPR003006; Ig_m
Pfam; PF00047; Ig; 2.
SMART; SM00408; IGC2; 1.
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CARBOHYD
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SIMILARITY: Belongs to the immunoglobulin superfamily. SIGL (SIALIC ACID BINDING IG-LIKE LECTIN) SUBFAMILY.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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                                                                                                                                         VISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLS
                                                                                                                                                                                                                                             RGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPLLWA----GCLATDG-YSLSVTGSVTVQEGLCVFVACQVQYP----NSKGPVFGYWF
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  WERPTQ -- KPFQLSTPAELQLPRAELEDQGKYICQAQNSQGAQTASVSLSIRSLLQLLGP
                                                     WTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121
                                                                                                                                                                                                                 SSALTSLGHRTTLS--SELNLTPRPQDNGTNLTCQVNLPGTGVTVERTQQLSVIYA----
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Ig_c2.
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                                                                                                          PQKMTIRVSWGDDTGTKVLQSGASLQIQEGESLSLVCMADSNPPAVLS
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IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
ITIN MOTIF.
SLAM-LIKE MOTIF.
BY SIMILARITY.

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Pred. No. 4.1
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EXTRACELLULAR (POTENTIAL
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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smatches 178;
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C2-TYPE 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 173;
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MGD; MGI:99440;
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  IPR003599;
                           IPR007110;
                                                       Cd33.
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MEDLINE-94250900; PubMed-8193354; Tchilian E.Z., Beverley P.C., Young "Molecular cloning of two isoforms of myeloid CD33 antigen."; Blood 83:3188-3198(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD33_MOUSE STANDARD; PRT; 403 AA. Q63994; Q63997; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Myeloid cell surface antigen CD33 precursor (Siglec-3).
                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
EMBL; S71345; AAB30842.1; EMBL; S71403; AAB30843.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/c; TISSUE-Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 33-A AND
                                                                                                                                                                                                                                                                                    ISOId-Q63994-2; Sequence-VSP_002534;
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIGLEC
(SIALIC ACID BINDING IG-LIKE LECTIN) SUBEAMILY.
SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                    European Bioinformatics Institute. The by non-profit institutions as long a lifted and this statement is not removed. It is requires a license agreement (See I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells that mediates sialic-acid dependent binding to cells. Preferentially binds to alpha2,6-linked sialic acid (By similarity). The sialic acid recognition site may be masked interactions with sialic acids on the same cell surface. SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS:
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                                                                                        SEQUENCE FROM N.A. MEDLINE-89392063; Pub Sato S., Fujita N., F Miyatake T.;
"cDNA cloning and glycoprotein."; Biochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Myelin-associated glycoprotein precursor (S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rPro, 19; 2
; PF00047; 19; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLV 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAXAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VREPFVRYSYKKSQLSLHVTSLSRTPDIIIPGTLEAGYPSNLTCSVPWACEQGTPPTFSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRKGVSLHEDSPVATSDPRQLVQKATQGRFQLLGDPQKHDCSLFIRDAQKNDTGMYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                                                                                                 (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
      Res.
                                                                amino
                                                                                                                                                PubMed=2476987;
                                                                                                                                                                                                                                                                    Chordata;
Primates;
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                                                                                                                    Kurihara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NVTRKSGQMRELVLVAVGEATVKLLILG--LCLV
   Commun.
                                                       acid sequence
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

OF SI
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Pred. No. 5.7e-30;
                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROBAITSYNHCLISPTASDAVTPGCSIHRLISRTPRCTAILR
IQDPYRTHLKNRAVSTLREPMISWEGSLRSTORSKCTKLC
SPYKNLCPLWLPVDNSCIPLIPEWYNLLCVSLTLS -> AFO
QODSKVHSNPENPRPLQKDSPQEQSSVHTKISLDEMGGKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYSEI (in isoform 33-A).
/FTId-VSP_002534.
F1FE6D5C393F0FF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
163:1473-1480(1989)
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                                                                                                                                                                                                                                                                                                                                                                                  precursor (Siglec-4a).
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                                                                                                                 Kuwano
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                                                          for
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                                                                                                                    R.,
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                                                          human myelin-associated
                                                                                                                 Sakimura
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                                                                                                              Takahashi
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Query Match
Best Local
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LIPID
SEQUENCE
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DOMAIN
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Pfam; PF00047; Ig; 2.
SMART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Cell adhesion; Lectin; Transm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by said an one of send and send an one of send and send an one of send and send an o
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SEQUENCE FROM N.A.
LAMERTIN J.E., McCready P.M., Adamson A.W.,
LAMERTIN J.E., McCready P.M., Adamson A.W.,
Kyle A., Ramirez M., Stilwagen S.A., Garnes
Bruce R., Quan G., Montgomery M., Ow D., Kob
Carrano A.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M29273; AAA59545.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 159460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A61084; A61084.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lmmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q62230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
             al Similarity
137; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC: 6783; MAG.
                                                                                                                  454
531
626
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                                                                                                               531 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Signal; Glycoprotein;
Score 303.5; DB 1;
Pred. No. 5.7e-14;
Pred. No. 5.7e-14;
                                                                                                                                                              IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 4
IG-LIKE C2-TYPE 4
BY SIMILARITY
N-LINKED (GLCNAC,
N-LINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                             PALMITATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYELIN-ASSOCIATED GLYCOPROTEIN EXTRACELLULAR (POTENTIAL).
                                                                                                                  ED2D36B24F21CAAA
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(GLCNAC...)
(GLCNAC...
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Kobayashi A., Olsen
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                                                                                                                                        SIMILARITY).
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J., Danganan L.,
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                                                                                                                  CRC64;
                                                          Length
                                                                                                                                                                                       (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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                                                          626;
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Q92154;
15-JUL-1998
15-JUL-1998
15-SEP-2003
                                                                                                                                                         Roder J.
                                                                                                                                                                                                                                                                                                                                                     SMP.
                                                                structural similarities within the immunoglobulin superfamily Neuron 8:323-334(1992).
-I- SUBCELIULAR LOCATION: Type I membrane protein.
-I- TISSUB SPECIFICITY: Exclusively expressed by myelinating
                                                                                                                                                                                                                                                                                                                 Coturnix coturnix japonica (Japanese quail). Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                               SEQUENCE FROM N.A.,
563-571.
                                                                                                                                                                                                                                                                                                                                                                 Schwann cell myelin protein precursor
                                                                                                                                           "Molecular characterization of the
                                                                                                                                                                                           MEDLINE-92153423; PubMed-1739462;
                                                                                                                                                                                                                                                                                                Archosauria; Aves;
                                                                                                                                                                                                                                                              NCBI_TaxID-93934;
                                  nonmyelinating schwann cells and oligodendrocytes. DEVELOPMENTAL STAGE: First synthesized at embryonic
 remains expressed SIMILARITY: BELONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCAAARDTVQCLCVVKSNPEPSVAFELPSRNVTVNESEREFVYSERSGLVLTSILTL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEPAVLGRLREDEGTWVQVSLLHFVPTREANGHRLGCQASFPNTTLQFEGYASMDVKYPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --- AALSS-QGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFSEH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAIVCYITQTRRKKNVTESPSFSAGDNPPVLFSSDFRISGAPEKYESERRLGSERRLLGL
                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 36, Created)
(Rel. 36, Last sequence up
(Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                               ; Chordata; Craniata; Vertebrata; Euteleostomi; Neognathae; Galliformes; Phasianidae; Phasiani
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   IMMUNOGLOBULIN
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                                                                                                               schwann cell myelin
immunoglobulin super
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   SUPERFAMILY.
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   SIGLEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
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HSSP; P56276; 1TLK.
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Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig;
SMART; SM00408; IG:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
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                  PENLRVMVSQAN----
                                                                                    GVSAQRTVRLRVAYAPR----
                                                                                                                                                     CPP--PSFSWTGA--ALSSQGTK-----PTTSHFSVLSFTPRPQDHDTDLTCHVDFSRK
                                                                                                                                                                                         AGKYYFRGDLGGYNQYSF-SEHAELDVWA---APHLEVPHELVAGSEAEILCRVP---DN
                                                                                                                                                                                                               -SQYFFRVERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEE
                                                                                                                                                                                                                                                              -----FGSPYPKNYPPVVARSRPSSAVHESFAGRASFLGDPTGRDCTLNI--ARLSEEL
                                                                                                                                                                                                                                                                                                AVTETTKGAP-----VATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDE-
                                                                                                                                                                                                                                                                                                                                   LVLTVLLMGTGCISAPWAAWMPPKMAALSGTCVQLPCRFDYPEE----LRPASIGGLWY-
                                                                                                                                                                                                                                                                                                                                                                   LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAY--GYWFK
                                                  SLSFQADVGLDVQYEPQVVGLWGPTEVVEGSDVELGCEAEGRPAPLISWFRGSEVLREEP
                                                                                                                        CPPLRPLLTWTGTEELLDPIGKERIEDDLGSKSLLGSLRFRPRKEDLGRRVGCGVTFINS
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IPR003598;
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Ig_c2.
Ig_MHC.
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IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 4
BY SIMILARITY
BY SIMI
                     RTVLEN
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9; Mismatches
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5.6e-14;
hes 224;
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                   -LGNGTSLPVLEGQSL
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Db	284	284 GRNLRLLLSNVGPDDGGSFSCVAENRHGRHNRSLQLRVAYAPRAPVING-SLWVVSGDPV 342	
Qy	287	287 CLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHV 346	
Db	343	343 SYTCRAESEPAAILTVLRGGKVMAAAIYEDHYTMEMRPARPEDGGTYSCVAENQHGASST 402	
Qy	347	- 70	
DЪ	403	403 SFNISVEYPPLVLPASRCTAGGDGVRCVCMVNSIPDSSLVFELPTRNQTVSDGHRDFTAA 462	
Qy	364	SNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRH 406	
ф	463	463 PPGSDGSITGI-LTLRGPLEPRLLVLCAARNRHGTTARQLRFHHPGGLVWAK 513	
Qy	407	407STILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQ 452	
Db	514	514 VGPVGAVVAFAIVIAVVCYLSQSRRKKGAGSPEVTPVQPMAGPGGDPDLDLRPQQVRWLR 573.	
Qy	453	,PSFPE	
Db	574	GAMERWALGVKEGSGAPQEVTPTSHPPMKPTRGPLEDPPEYAEIR 618	

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                          Q95kp8 pongo
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Q9d4m0 homo
                                                                                               Q8btg2 mus 1
Q8iw38 homo 1
Q8bu57 mus 1
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1151 1174	467	373	5636	494	1217	1041	335	213	739	739	650	412	1256	1256	1256	1332	1332	718	468	464	662	510	1252	510	577	483	402
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Q9qvn5 rattus sp. Q91z60 rattus norv	homo	homo	Q96rw7 homo sapien	Q9esc6 mus musculu	5 rat	homo				Q28260 canis famil	Q9gkr2 bos taurus	. Q8hyl4 oryctolagus	Q9et59 mus musculu	Q9jix1 mus musculu	Q925s5 mus musculu	Q9vqw7 drosophila		caen		homo	g o	Q96k15 homo sapien	ratt	OMO	Q9d2zl mus musculu	Q9dbp8 mus musculu	O35444 mus musculu

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8BY18 PRELIMINARY; PRT; 623 AA.
Q8BY18;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Meakly similar to sialic acid-binding lectin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK042488; BAC31272.1; -.
SEQUENCE 623 AA; 69384 MW; 5827C09D52C3AC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRALN=C57BL/6J; TISSUE=Thymus;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-10090;
122 RGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSWT
                                                                                                                                                                                     62 KAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 Similarity 43.1 267; Conservative
                                                                                                                                         63 KGIRKPSLSFPVATNNKDKVLEWEARGRFQLLGDISKKNCSLLIKDVQWGDSTNYFFRME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.8%; Score 1211.5; DB
43.1%; Pred. No. 1.3e-96;
tive 55; Mismatches 111
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC035809; AAH35809.1; -.
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
SIGLEC-like 1.
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Q81YH7;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
     SQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISIS
                                                                            KWNYIYDKLSVHYTALTHMPTFSIPGTLESGHPRNLTCSVPWACEQGTPPTITWMGASVS
                                                                                                             TTKGAPVATNHOSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYV 126
                                                                                                                                                                             IPWDIPVATNTPSGKVQEDTHGRFLLLGDPQTNNCSLSIRDARKGDSGKYYFQVERGSR-
                                                                                                                                                                                                                                                                                                           LSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFKAVTE
                                                                                                                                                                                                                                                                            LSVNVTASQDLLSRYRLEVPESVTVQEGLCVSVPCSVLYPHYNWTASSPVYGSWFKEGAD
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65; Mismatches 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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     Q8IW38;
01-MAR-2003
                                                     Q81W38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBBTG2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Weakly similar to sialic acid-binding lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Bone; MEDLINE=22354683; PubMed=12466851; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK036698; BAC29538.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8BTG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                         RGSYVRYNEMNDGEFLKVTALTQKPDVYIPETLEPGQPVTVICVENWAFEBCPPPSFSWT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLPLLLSSLLGGSOAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWF
                                                                                                                                                                   GDAVSFQESRPHTSNYSVLSFIPGLQHHDTELTCQLDFSR--MSTQRTVRLRVA
                                                                                                                                                                                                                                                               RG-FERFSFKEE-FRLQVEALTQKPDIFIPEVLEPGEPVTVVCLFSWTFNQCPAPSFSWM
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  (TrEMBLrel.
                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.5%; Score 664; DB 11;
55.1%; Pred. No. 1.7e-49;
56. Mismatches 65;
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23,
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on functional
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Matches 134
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Oviduct;
STRAIN-C57BL/6J; TISSUE-Oviduct;
MEDLINE-22354683; PubMed-12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
*Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs.";
Nature 420:553-573(2002).
RMBL; AK087658; BAC39955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBBU57;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sialic acid-binding lectin SIGLEC-F homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ
EMBL; BC041072; AAH41072.1; -.
NON_TER 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Similar to CD33 antigen (gp67) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                             134; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPCSFSYPRQDWTGSTPAYGYWFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAK 98
                                  NCSLVIRDAQMQDESQYFFRVERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FPGAGVTTERTIQLSVSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSRKGVSAQRTVRLRVAY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSNLTCSVPWVCEQGTPPIFSWMSAAPTSLG--PRTLHSSVLTIIPRPQDHGTNLICQVT 240
NCSLDIRDAQKIDTGTYFFRLD-GS-VKYSFQKSMLSVLVIALTEVPNIQVTSTLVSGNS
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                                                                                                                                                                                                                                                                                               423 AA;
                                                                                                                                             17.4%;
llarity 29.3%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Chordata;
; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33416 MW;
                                                                                                                                                                                                                                                                                               45208 MW;
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Pred. No. 8e
                                                                                                                                             Score 471.5; DB 11
Pred. No. 1.7e-32;
9; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A21DF49DAC3CB85B CRC64;
                                                                                                                                                                                                                                                                                           7393D0E4BE5BF455 CRC64;
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                                                                                                                                                                                                              DB 11; Length 423;
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Best Local
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 1.
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-- PRTLHSSELTIIPRPQDHGTNLICQVTFPGAGVTTERTIQLSVSW
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SEQUENCE FROM N.A.
MEDLINE-21523976; PubMed=11546777;
Angata T., Varki N.M., Varki A.;
"A second uniquely human mutation affecting
J. Biol. Chem. 276:40282-40287(2001).
                                                                             Q95KQ0 PRELIMINARY; PRT; 271 AA. Q95KQ0; Q95KQ0; Q1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) 51alic acid-binding lectin Siglec-L1 (Fragment). Pan paniscus (Pygmy chimpanzee) (Bonobo). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID-9597;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Stalic acid-binding lectin Siglec-L1 (Fragment).
Gorilla gorilla (gorilla)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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EMBL; AY029754; AAK50563.1; JOINED.
InterPro; IPR003599; Ig-
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
Defan. Pro0047.
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Angata T., Varki N.M., Varki A.;
Angata T. Varki N.M., Varki A.;
A second uniquely human mutation affecting
J. Biolo. Chem. 276:40282-40287(2001).
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                                                                                                                                                                                                                                                                                                                            EECPPPSFSW--TGA-----ALSSQGTK---PTTSHFSVLSFTPRPQDHDTDLTCHV
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                                                                                                                                                                                                                                                                                                                                                                                                       FRAGDHVSRNVPVATNNPARAVQEETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYVFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
269 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                                                                                                                                                                                                                 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%; 37.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 360.5;
Pred. No. 4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96E49E4F779D6E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
               sialic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sialic acid biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
               acid
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                                                                                                    Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorilla
               biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 9
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Best Local
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Interpro; IPR003006; Ig_MHC.
Pfam; PP00047; 1g; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835.
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Best Local
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00409; IG; 2.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   *Angata T., Varki N.M., Varki A.;

*A second uniquely human mutation affecting
J. Biol. C.hem. 276:40282-40287(2001).

EMBL; AY029757; AAK50564.1; -.

EMBL; AY029756; AAK50564.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus (Orangutan),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
NCBI_TaxID-9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC 2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update 01-MAR-2003 (TrEMBLrel. 23, Last annotation update stalic acid-binding lectin Siglec-L1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21523976; PubMed=11546777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95KP8;
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                                                                            90; Conservative
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MLLPLLLSSLLGGSQAMDGREWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGDHVSRNVPVATNNPARAVQEETRDRFHLLGDPQNKDCTLSIRDTRESDAGTYVFRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EECPPPSFSW--TGAAL-----SSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHV
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269 /
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271 AA;
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30649 MW;
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30613 MW;
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36.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                          Score 351.5; DB 6;
Pred. No. 2.5e-22;
2; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 358.
Pred. No.
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                                                                                                                                                                        D21277346EC3C7CA CRC64;
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No. 6.1e-23;
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                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          biology.";
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                                                                          Gaps
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"Isolation of novel full-length
libraries.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 34.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein. SEQUENCE 312 AA; 34610 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AB070150; BAB63095.1; -.
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Hashimoto K., Osada N., Hida M., Kusuda J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecinae; Macaca.
NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       ### HTGNLDEEDCTLLIHDILKGNSATYLFYADLGEQ-KSAFLGENIKLFVSDLTQKPELHIP
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      LAQKRNQKATPNSPRTPLPP 441
                                       GAIAFSLLFFCLVLLLMKMLNWWEEHQSPKTKEGLTLKKPELLEEPEV-------
                                                                            GITA--LLFLCLALIIMKIL------PKRRTQTETPRPRESRHSTILDYINVVPTAGP
                                                                                                                                                                                                                                        LGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE-LPRV----
                                                                                                                                                                                                                                                                                    TLGCHLNFSLANVTRSSLVKLQVVSPHRLFNSSCS-----------
                                                                                                                                                                                                                                                                                                                     DLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLEN
                                                                                                                                                                                                                                                                                                                                                              EILLAEKPVALNCTLKGTCKEIKALFRSRKNPAVSS-----SSSSVPHFILRPEDHGN
                                                                                                                                                                                                                                                                                                                                                                                                    ETLEPGQPVTVICVFNWAFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFSRKGVSAQ 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                        VPWANSTINLIGEPEIVMRLRCEGKNQYGI-HTSSFFLIPNKKS-VSSMFVKGLIQGIVY
                                                                                                                                                             RDARKGDSGK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SS--PVYGSWFKEGADIXWDIPVATNTPSGKVQEDTQGRFLLLG---DPQTNNCSLS--I 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EECPPPSFSW--TGAAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERGN-IKWSYKHDQLSVNVTASQDLLSRYRLEVPESVTVQEGLCXYVPCSVLYPHYNWTA
                                                                                                                                                                                                   ------LEKTVLC-SCSFHGIPTPSVQWWMGG-----VPVDVNSMDNIPRVTSSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLPPLLCGRVGAKEQKD--YLLTMQKSVTVQEGLCVSVLCSFSYPQDDWTDSDPVHGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3.60
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 235.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42CA54C314CC1CF0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103;
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Best Local S
Matches 124
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01-NOV-1996
01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00019; ACTININ_1; 1.

PROSITE; PS00035; IQ_LIKE; 2.

Alternative splicing; Immunoglobulin domain; SIGNAL 1 34 POTENTIAL.

CHAIN 35 430 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan Kobayashi A., Olsen A.S., Carrano A.V.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X14831; CAA32940.1; -. EMBL; AC004785; AAC18435.1; -. InterPro; IPR0073189; Actbind_actnin. InterPro; IPR007110; Ig-1ike.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W., Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S Burkhart-Schultz K., Gordon L., Kyle A., Garnes J., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Carcinoembryonic antigens: alternative splicing accounts for the multiple mRNAs that code for novel members of the carcinoembryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00213; MYELINPO. SMART; SM00408; IGC2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barnett T.R., Kretschmer A Elting J.J., Kamarck M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TM2-CEA
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000920; Myelin_P0
Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen
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MEDLINE-89139550; PubMed-2537311;
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les 124;
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                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.
FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                            QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY----
                                                                                                                                                                 GY-WFKAVTETTKGAPVATNHOSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                     LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ------LF
                                                                                             MODESQYFERVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA
                                                                                                                                           GYSWYKG-
                                                                                                                                                                                                                                                           LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
                                                                                                                                                                                                                                                                                                                                                                                 430
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                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108:267-276(1989).
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                                                                                                                                                                                                                                                                                                                                                                               430 F
46910 MW;
                                                                                                                                                                                                                                                                                                7.6%; Score 205; DB 4; 22.6%; Pred. No. 2.5e-09; Live 73; Mismatches 174
                                                                                                                                         -----NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                 195DE9F171D1414F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal;
                                                                                                                                                                                                                                                                                                                                          Length 430;
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                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane
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                                                                                                                                                                                                                                                                                                    178;
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121;

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ACCOMPAND ACCOMP
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Q9D4M0
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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
A Fleischmann W., Gaasterland T., Misio B., Kochiwa H.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazazarelli J., Mombaerts P.,
A Mordone P. Rainchioni L., Mashima J., Mazazarelli J., Mombaerts P.,
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         Query
                                                                                                                                         MGD; MGI:1921304; 4931406B18Rik.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                    "Functional annotation of a full-length Nature 409:685-690(2001).
NATURE 409:685-690(2001).
                                                                                                                                                                                                                                                                          Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                 Pfam; PF00047;
                                                                                                                                                                                                                                                                Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21085660; PubMed=11217851;
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01-MAR-2003
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                                 ); 15; 19; 2.
F00047; 19; 2.
S; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM N.A.
57BL/6J; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIYSEVKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRP-RPEARMPK--GTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPL-GSQHVSLSLSVHYKKGL-ISTAFSNGAFLG--IGITALLFLCLALIIMKIL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRASDQRDLTE-HKPSVSNHTQ--DHSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSVTGCNRTTVKTIIVTDNALPQENGLSPGAIAGIVIGVVALVAL-IAVALACFLHFGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYRPGANLSLSCYAASNPPAQYSWLINGTFQQSTQE-----LFIPNITVNNSGSYTCHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRLRVAYAPRDL-VISISRDNTPDPPENLRVMVSQANRT--VLENLGNGTSLPVLE----
                                                                                                                    IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---PKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PELPKPS---
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       7.3%;
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17,
23,
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Last annotation updat
       Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                             24CAADEA63F47F95 CRC64;
       198.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---EVTYSTLNFEAQQPTQPTSASPSLTATE
                                                                                                                                                                                                                                      mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
       DВ
       11;
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    Length
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Matches 102; Conservative
                                                                                                                                                                                                                             Kuroki M., Matsuo Y., Misumi Y., Oikawa S., M
"A new isoform of human biliary glycoprotein
encoded by an Alu-like sequence.";
                                                                                                                                                                                                                                                                                                                                                                                   Barnett I.A., M.E.;
Elting J.J., Kamarck M.E.;
"Carchoembryonic antigens: Alternative splicing a
"Carchoembryonic antigens: Alternative splicing a
                                          InterPro; IPR003006; I
Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2;
                                                                                                                                                                                                                                                                                                                                                                       multiple mRNAs that code antigen family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barnett T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=89139550; PubMed=2537311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                       Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biliary
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01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q13854;
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                       PROSITE;
                                                                                                               InterPro; IPR003598;
                                                                                                                                     InterPro; IPR001589;
InterPro; IPR007110;
                                                                                                                                                                                    EMBL; D12502; BAA02063.1;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      341
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                       PS00019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPA--KGNCSLVIRDAQMQDESQYF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLLPL-LLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKRRT - - QTETPRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FHGIPTPLVQWWVGGTPVSVNRID--GILHLTTTLE---PWTNSTIHLIWEPKIILTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLYLGLLSPVL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEGKNQYGVHASRTFLIPDKSSVSSVFLRGLIQGIVYGAIASALFLFFLVVLVMKMLNWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----SVHYK------KGLISTAFSNGAFLGI---GITALLFL-CLALIIMKIL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALFLSWKGPIMSSNTTISIHPS----SALAIELKPEDQGTTLRCHLKLSLDNLSSSKVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILMTH-SMLRRKYMTNSLYVGLGTQKDLTQNPELHIPESSVAGEPVTLSCTIQSTCQEPN 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRVAYAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -YKAPFRN----PMAVSYRLNE-NISFRVG---TSHPSAPMGDLS----TEEVEYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             108:267-276(1989).
ACTININ_1; 1. IG_LIKE; 2.
                                                                                                             Ig-like.
Ig_c2.
                                                                                        Ig_MHC
                                                                                                                                                          Actbind_actnin
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01,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 7.5

in Mismatches
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les 146;
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                                                                                                                                                                                                                                                                            Matsuoka
                                                                                                                                                                                                                                                     (BGP)
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accounts for

carcinoembryonic

containing

α domain S.J.,

Hart J.T.,

Euteleostomi;

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RESULT
O60430
O60
D7 O60
D7 O10
D7 O11
D7 O1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998
01-AUG-1998
01-MAR-2003
SEQUENCE FROM N.A.

Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

Lamerdin J.E., McCready P.M., Kyle A., Ramirez M., Stilwagen S.,

Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,

Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,

Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,

Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,

Kronmiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.

Kobayashi A., Olsen A.S., Carrano A.V.;

"Sequence analysis of a 2.5 Mb region in 19q13.2 containing a

clustered CEA/PSG gene family.";
                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BGP_HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      060430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYSWYKG--ERVDG-----NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQEELHYATLNFPGVRP-RPEARMPK--GTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAFLG--IGITALLFLCLALIIMKIL-----PKRRTQTETPRPRFSRHSTILDYINV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
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B (TrEMBLrel.
CTrEMBLrel.
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21.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local
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                                                                                                                                                                                                         OBROO7;

O1-JUN-2002 (TrEMBLrel 21, Created)

O1-JUN-2002 (TrEMBLrel 21, Last seq

O1-MAR-2003 (TrEMBLrel 23, Last ann
                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                      Similar to poliovirus receptor-related Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                    Q8R007
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InterPro; IPR007110; Ig-like.
                          SEQUENCE FROM N.A
                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Similarity 21.2%;
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                                                                                                                                                                                                                                                                                                                    PRT;
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases EMBL; AC004785; AAC18433.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYSWYKG--ERVDG-----NRQIVGYAIGTQQATPGPANSGRETIYPNASLLIQNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVP-----CSFSYPRQDWTGSTPAY
                                                                                                                                                                                                                                                                                                                                                                                            KMNEVTYSTLNFEAQQPTQPTSASPSLTATEIIYSEVKKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQEELHYATLNFPGVRP-RPEARMPK--GTQADYAEVKFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIGVVALVALIAVALACFLHFGKTGRASDQRDLTEHK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RLQLSNGNRTLTLLSVTRNDTGPYECEIQNPVS-ANRSDPVTLNVTYGPDTPTISPSDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -PELPKPS----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -PRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGA----
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Pred. No. 2.3e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like. InterPro; IPR003598; Ig_C2. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; 'ig; 2. SMART; SM00408; IGC2; 1. PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin domain; Receptor. SEQUENCE 508 AA; 55657 MW; 24D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC024948; AAH24948.1; -. EMBL; BC024948; AAL79833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.; "NectLn4/PRR4, a new afadin-associated member of the nectin family that trans-interacts with nectin1/PRR1 through V domain interaction."; J., Blol. Chem. 276:43205-43215(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=21560925; Pubmed=11544254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases [2]
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395 SIRR-LHSHHSDPRSQPEESVGLRAEGHPDSLKDNSSCSVMSEEPEGRSYSTL 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 AKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 -RGDPDEQVGQVAWARVDPNEGIRELALLHSKYGLHVNPAYEDR-VEQPPPPR-----DP
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                               SPRTPLPPGAPSPESKKNQKKQYQLPSFPEP-KSSTQAPESQESQEELHYATL 485
                                                                LLFCLLVVVVVLM-----SRYHRRK------AQQMTQKYEEELTLTREN
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                                                                                                                                                                                                                                            QANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLEL 322
                                                                                                                                                                                                                                                                                   SRSMNGQPLTCVV--SHPGLLQDRRITHTLQVAFLAEASYRGLEDQN------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPLSLGAEMWGPEA----WLRLLFLASFTGQYSAGELETSDVVTVVLGQDAKLPCFY--
                                                                                                    LFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKAT---PN 433
                                                                                                                                                                                                                                                                                                                RPQDHDTDLTCHVDFSRKGVSAQR--TVRLRVAYAPRDLVISISRDNTPDPPENLRVMVS
                                                                                                                                                                                                           -----LWQVGR-----EGAT--LKCLSEGQPPPKYNWTRLDGPLPSGVRVKGDTLGF 301
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Search completed: October Job time: 68 secs

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2706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
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US-09-038-832-2
US-09-046-736-2
US-08-759-628-4
US-08-759-628-5
US-08-759-628-5
US-08-640-736-4
US-08-640-736-4
US-08-602-725-32
5169835-17
US-09-638-649-1
US-09-638-649-1
US-09-638-649-1
US-08-217-229-1
US-08-98-622-725-36
US-08-98-859A-17
US-09-77-802-10
US-09-778-510-2
US-09-778-510-2
US-09-778-510-2
US-09-778-825-4
US-09-778-825-14
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                                                                                                    CURRENT APPLICATION NUMBER: US/09/038,832

FILING DATE: 11-MAR-1998

CLASSIFICATION E 11-MAR-1998

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/041,886

FILING DATE: 02-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: PRESTIA, PAUL F

REGISTRATION NUMBER: 23,031

REFERENCE/DOCKET NUMBER: GH-50018

TELECOMMUNICATION INFORMATION:

TELEFAN: 610-407-0701

TELEFAX: 610-407-0701

TELEX; 846169

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 431 amino acids

TYPE: amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
                                                                                          ; MOLECULE TYPE: US-09-038-832-2
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US-09-038-832-2
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                     Matches 195;
                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ERICKSON-MILLER, CONNIE TITLE OF INVENTION: SIALOAdhesin ReTITLE OF INVENTION: (SAF-2) NUMBER OF SEQUENCES: 4
ANDERSCREE BANKER & BESCHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. BOX 9
CITY: VALLEY FORGE
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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US-08-750-141A-2
PCT-US93-00031-23
US-08-261-304-2
US-08-266-206B-21
PCT-US95-08493-13
US-09-724-864-6-8
US-08-359-705B-6
US-08-457-880A-8
US-08-457-880A-6
2 US-08-359-705B-6
2 US-08-359-705B-6
2 US-08-359-705B-6
2 US-08-359-705B-6
2 US-08-359-705B-6
2 US-08-359-705B-6
                     52;
                                      Score 888; DB 3; Pred. No. 9.8e-70;
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                     Mismatches
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Length 431; Indels

34;

Gaps

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US-09-038-832-4
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Patent No. 6146845
GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TIFLE OF INVENTION: Sialoadhesin Family Member-2
TIFLE OF INVENTION: (SAF-2)
                                                                                                      TELEX: 846169
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
            MOLECULE TYPE:
                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0
FILING DATE: 02-APR-1997
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/038,832
FILING DATE: 11-MAR-1998
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
CITY: V
                                TOPOLOGY: 11
                                                                                  LENGTH:
                                                                                                                                                                                                                    NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50018
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
SOFTWARE: FastSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: RATNER & PRESTIA STREET: P.O. BOX 980
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                                                                  amino acid
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                                                                                431 amino acids
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US-09-046-736-2
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                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: KIKLY,
APPLICANT: ERICKSC
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                                                                                                                                              APPLICATION NUMBER: 60/04
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestla, Paul F
                                                                      REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                        CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Sialoadhesin Family Member-3 NUMBER OF SEQUENCES: 4
                                                        TELEFAX:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0
FILING DATE: 24-MAR-1998
                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 VRLDVSY-------PPWNLTMTVFQGDATASTALGNGSSLSVLEGQSLRLV
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al Similarity 47.8%;
195; Conservation
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                                                      610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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O. Box 980
                                                                                                                                                                                                                                                                                                                                                                                    Diskette
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RESULT 4
US-08-759-628-4
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                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08759628 Patent No. 6225446 GENERAL INFORMATION:
                                                                                                                                                                                 APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MANUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                          COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                      STREET: 901 Califo
CITY: Palo Alto
STATE: California
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   APPLICATION NUMBER:
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Pred. No. 1e-64;
8; Mismatches 174;
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US-08-759-628-5
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Best Local Similarity
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                GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEPAX: 415-496-1200
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NUMBER OF SEQUENCES:
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36.5%; Pred. No. 2.8e-59;
tive 73; Mismatches 163;
                  MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
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              Sequence 4, Application US/09046736 Patent No. 6090582
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GENERAL INFORMATION:
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FILLING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX05520
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTANDED: PARCETTE POLICIES #100
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ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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STRANDEDNESS: si
TOPOLOGY: linear
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STATE: Californ
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                                                                                                                                                                LSWFQGSPALNATPISNTGILELRRVRSAEEGGFTCRAQHPLGFLQIFLNLSVYSLPQLL
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Pred. No. 1.1e-52;
3; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
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REGISTRATION NUMBER: 23
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                           296 PPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHYK 355
                                                                                                                                                                                     236 YAPRDLVISISRDNTPDPPENLRVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSS 295
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156; Conserv
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                             YTGKMRPVSGVLL-----GAVGGAGATALVFLSFCVIFIVV---RSCRKKSARP-----
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TILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSS
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                                                                                                                                                                                                                                                                                                                  YFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPP 175
                                                                                                                                                                                                                                                                                                                                                                     MLLLLLLPLLWGRERVEWQKSNRKDYSLTMQSSVTVQEGMCVHVRCSFSYPVDSQTDSDP
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                                                         -----KGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHS
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O. Box 980
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24-MAR-1998
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Pred. No. 3.6e-42;
3; Mismatches 138;
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US-08-408-095-31
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,095
FILING DATE: 21-MAR-1995
CLASSIFICATION: 435
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NAME: Mack, Susan J.
REGISTRATION UNMBER: 30,951
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
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TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
NUMBER OF SEQUENCES: 35
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CITY: Washington
STATE: D.C.
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 292
                                 314 PSDPGVLELPRVQVEHEGEFTCHARHPLGSQHVSLS-LSVHYKKGLISTAFSNGAFLGIG 372
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                                                                                                                                                                                                                      KPLSE-----IHSGNSVSLQCDFSSSHPK--EVQFFWEKNGRLLG----KESQLNF 212
                                                                                                                                                                                SVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPDPPENL
                                                                                                                                                                                                                                                               TALTOKPDVYIPETLEPGOPVTVICVFNWAFEECPPPSFSW--TGAALSSOGTKPTTSHF 197
                                                                                                            RVMVSQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPAR----LSWTQRGQVLSPSQ 313
                                                                                                                                                 DSIS----PEDAGS-YSCWVNNS-IGQTASKAWTLEVLYAPRRLRVSMSPGD------
                                                                                                                                                                                                                                                                                                                                    REVEMSTRGREQLTGDPAKGNCSLVIRDAQMQDESQYFFRVERGSYVRYNFMNDGFFLKV 139
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PHHSQKLRLEPVKVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETI-----GRRVAVG
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(202)293-7860
31:
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                                                                        -----QVMEGKSATLTCESDANPPVSHYTWFDWNNQ-----SL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Mismatches 182;
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; TYPE: PRT
; ORGANISM: Murine
US-09-638-649-5
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US-09-638-649-5
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SOFTWARE: PatentIn Vo
SEQ ID NO 5
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GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 0575/62175
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CURRENT FILING DATE: 2000-08-14
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                                 ----QSEEAEMPE
                                                                        PGVRPRPEARMPK
                                                                                                                                                                                                                          FLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRN 427
                                                                                                                                                                                                                                                                                  LPRVQVEHEGEFTCHARHPLGSQHVSLSLSVHY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVPNKVGTCVSEGSY---PAGTLSWHLDGKLLIPDGKETLVKEETRRHPETGLFTLRSEL
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                                                                                                                                               QKATPNSPRTPLPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNF 487
                                                                                                                                                                                                                                                                                                                                                                                                              TVIPTQGGTTHPTFSCSFS-LGLPRRRPLNT----APIQL-----RVREPGPPEGIQLLV 241
                                                                                                                                                                                    LGGLGVVALL----
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                                                                                                                                                                                                                                                                                                                                                                         SQANRTVLENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 403
                                                                                                            -APESQEDEEE--RAELN- 388
                                                                                                                                                                                    ----VGAILWRKR
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TYPE: protein
US-08-602-725-32
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US-08-602-725-32
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
CLASSIFICATION E30
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/08602725 Patent No. 5965710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 32:
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APPLICANT: BODMER,
APPLICANT: DURBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acid
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FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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ADDRESSEE: NIXON & V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-616-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 1
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                                                     142 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
                                                                                                                                                                   110 MQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWA 169
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                                                                                                                                                                                                                                             58 GY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDAQ 109
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22201
                                                                                           FEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRT
                                                                                                                                   QNDTGFYTLQV-----IKSDLVNE-----EATGQFHVY---
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                                                                                                                                                                                                                                                                                   LLTASLL-----TFWNPPTTAQLTTESMPFNVAEGKEVLLLVHNLPQQ------LF 63
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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DURBIN, HELGA
SNARY, DAVID
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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BATES, PAUL A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703-816-4091
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21-AUG-1993
                                                                                                                                                                                                                                                                                                                                                               6.2%; Score 167; DB 2; 1
23.5%; Pred. No. 2.1e-06;
ative 52; Mismatches 122;
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US-09-638-649-1
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APPLICANT: WAI-YEE, CHAN

TITLE OF INVENTION: PREGNANCY SPECIFIC

NUMBER OF SEQUENCES: 48

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/390,409
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5169835-17
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;SEQ ID NO:17:
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                                                 SOFTWARE:
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                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09638649 Patent No. 6563015
                                                                                                                                        APPLICANT: Stern, David M.
APPLICANT: Schmidt, Ann Marie
APPLICANT: Schmidt, Ann Marie
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED
TITLE OF INVENTION: GLYCATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AN
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 0575/62175
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Best Local Similarity
Matches 73; Conserv
                                                                                      CURRENT APPLICATION NUMBER: US/09/638,649
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 10
TYPE: PRT
ORGANISM: Bos Taurus
                                  LENGTH: 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58
                                                                     PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PELPKPS-----ISSNNSNPVEDKDAV-AFTCEPETQDTTYLWWINNQSLPVSP---
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US-09-996-243-503
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                                                                                    APPLICANT:
                                                                                                                                                        APPLICANT:
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730p1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 KAVTETTKGAPVATNHQSREVEMSTRGRFQL-----TGDP-----AKGNCSLVIRDAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi, Avi J.
Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQDEGTFRCRATSRSGKETKSNYR-----VRVYQIPGKPEIVDPASELMAGVPNKVGTCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVALL----
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                                                                                                Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                          Tumas,
                                                                                                                                                                    Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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FILING DATE: 1998-06-11
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DR FILING DATE: 1998-06-12
DR APPLICATION NUMBER: 60/01
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DR APPLICATION NUMBER: 60/01
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                                                                                                                  RVTVQYVQSIGMVA----GAVTGIVAGALLIFLLVWLLIRRKDKERYE-EEERPNEIREDA
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PRIOR APPLICATION NUMBER: 60/089908 PRIOR FILING DATE: 1998-06-18 PRIOR APPLICATION NUMBER: 60/089947 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089948 PRIOR FILING DATE: 1998-06-19

APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19

OR APPLICATION NUMBER: 60/089952
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090355 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/090429 FILING DATE: 1998-06-24

APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24

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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-06-17

RESULT 13 US-09-040-774-2 Sequence 2, Application Patent No. 6207811 APPLICANT: Tryggv APPLICANT: APPLICANT: Tryggvason, Karl Kestila, Marjo Lenkkeri, Ulla Mannikko, Minna US/09040774 Karl

APPLICATION NUMBER: 60

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60/090694 60/090690 60/090678 60/090676

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APPLICATION NUMBER: 60/090542 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090557 FILING DATE: 1998-06-24

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                     Sequence 1, Application US/08217299
Patent No. 5672513
GENERAL INFORMATION:
APPLICANT: Mach, J. P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1241 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 97
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
APPLICANT:
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CITY: Chicago
STATE: IL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/040,774 FILING DATE: 18 MAR 1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 89; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 SOYFFRVERGSYVRYNFMNDGFFLKVTA----LTOKPDVYIPETLEPGOPVTVICVFNWA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLLGLLTEGLAQLAIPASVPRGFW-ALPENLTVVEGASVELRCGVSTP-----GSAV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLLPLLLSSL--LGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYG
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                                                                                                                                                                                                                                                                                                                                                                                         PVLE-----SQSLCLVCVTH-SSPPARLSWTQRGQVLSP-----SQPSDPGVL 320
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                                                                                                                                                                                                                                                                                                                                     PVIEWPGLDEGHVRAGQSLELPCVARGGNPLATLQWLKNGQPVSTAWGTEHTQAVARSVL
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Pelegrin, A.
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ACTERISTICS:

ACTERIST
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REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 9
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Terskikh, A.
TITLE OF INVENTION: Carcinoembryonic Antigen Derivatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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ZIP: 07110
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                   399 PRPRESRHST--ILDYINVVPTAGPLAQKR-----NQKATPNSPRTPL 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNW 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 YGY-WFKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKG-----NCSLVIRDA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 FGYSWYKG--ERVDG------NRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNI 78
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                                                                                                                                                                            SYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQE----LFIPNITVNNSGSYTCQAH
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                                                                                                                                                                                                                             ---EGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEETCHAR 338
                                                                                                                                                                                                                                                                                 -- RLQLSNGNRTLTLFNVTRNDTASYKCETQNPVSARRSDSVILNVLYGPDAPTISPLNT
                                                                                                                        HPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET 398
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                                                                       ----DTGLNRTT----
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b; Pred. No. 0.00043;
53; Mismatches 143;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4091
TELEPAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB94/01816
FILING DATE: 19-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9317423
FILING DATE: 21-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,725
FILING DATE: 02-FEB-1996
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MEDIUM TYPE: Floppy disk
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APPLICANT: BATES, PAUL A
TITLE OF INVENTION: MONOCLONAL ANTIBODIES FOR USE IN
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
NUMBER OF SEQUENCES: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 36663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
ZIP: 22201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
              186
                                                                                           136
                                                                                                                                                               109 IQNDTGFYTLHVIKSDLV--NEEATGQFR----- 135
                                                                                                        169 AFEECPPPSFSWTGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQR 228
                                                                                                                                                                                                       109 QMQDESQYFFRVERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNW 168
                                                                                                                                                                                                                                                59 FGYSWYKG--ERVDG-----NRQIIGYVIGTQQATPGPAYSGREIIYPNASLLIQNI 108
                                                                                                                                                                                                                                                                                      57 YGY-WFKAVTETTKGAPVATNHQSREVEMSTRGREQLTGDPAKG-----NCSLVIRDA 108
                                      TVRLRVAYAPRDLVI-SISRDNTPD-PPENLRVMVSQANRTVLENLGNGTSLPVL---- 281
                                                                                VYPELPKPS-----ISSNNSKPVEDKDAV-AFTCEPETQDATYLWWVNNQSLPVSP-- 185
6, Application US/08602725 5965710
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DURBIN, HELGA
SNARY, DAVID
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                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                            5.3%; Score 143; DB 2; Length 698;
21.3%; Pred. No. 0.00049;
tive 53; Mismatches 143; Indels 126; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1090-8
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Db	Qy	Db	Qy	Ър	Qy
319	399	299	339	244	282
319 PKPFITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQL 367	399 PRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPL 439	299 NS	339 HPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTET 398	244 SYRSGENLNLSCHAASNPPAQYSWFVNGTFQQSTQELFIPNITVNNSGSYTCQAH 298	282EGOSLCIVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHAR 338

Search completed: October 8, 2003, 20:04:44
Job time: 26 secs

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Title:
Perfect score:
Sequence:
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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      25780.5
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1: //ggn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: //ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: //ggn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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5: //ggn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: //ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: //ggn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: //ggn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

10: //ggn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

11: //ggn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

12: //ggn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

13: //ggn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

14: //ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

15: //ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

16: //ggn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

17: //ggn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

18: //ggn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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18: //ggn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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2706
1 MLLPLLLSSLLGGS
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Gapop 10.0 , Gapext 0.5
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           MLLPLLLSSLLGGSQAMDGR......RPEARMPKGTQADYAEVKFQ
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Copyright (c) 1993 - 2003 Compus
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      US-09-910-600-28
US-09-910-600-8
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US-09-918-295A-259
US-09-978-192A-259
US-09-978-189-259
US-09-978-189-259
US-09-978-189-259
US-09-978-189-259
US-09-978-191A-259
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Sequence 28, Appl Sequence 149, App Sequence 259, App
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			Query M Best Lo Matches	19 19 19 20 21 22 22 23 24 25 26 26 27 27 28 29 30 31 31 31 31 33 34 40 41 40 41 41 42 45 45 45 45 45 45 45 45 45 47 47 47 47 47 47 47 47 47 47 47 47 47	16 17
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FFLK	APVATNHQSR APVATNHQSR	QAMDO QAMDO	5.4%; 3.2%; 7e 1	ptic 0 100 100 100 100 100 100 100 100 100	
VTALTQKP	REVEMST	GRFWIRVQI GRFWIRVQI	Score Pred. ; Mis	US-09-9 US-09-9 US-09-9 US-09-9 US-09-9 US-09-9 US-10-1	9 6 6
DVYIPET	RGRFQLTG	ESVMVP	2580.5 No. 3.5 matches	16 10 16 16 16 16 16 16 16 16 16 16 16 16 16	978-6 918-5 918-4
	TGDPAKGI TGDPAKGI	EGLCISV	; DB 1 9e-195; s 1;	93A-259 93A-259 87B-259 87B-259 98A-259 98A-259 98A-259 98A-259 98A-259 98A-259 99A-118 99A	5 5 5
VTVICV	NCSLV	VPCSFSY VPCSFSY	1;	ence:	
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181 181 121

240 240 ERGSYVRYNFMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVFNWAFEECPPPSFSW 180

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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: pF489p2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-19
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1909-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1998-10-28
NUMBER: FILING DATE: 1998-10-28
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                                                                                                           ; TYPE: PRT; ORGANISM: Homo sapiens US-09-984-130-149
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US-09-984-130-149
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149, Application US/0984130 Publication No. US20030055231A1 GRMERAL INFORMATION: APPLICANT: Ni et al.
                                                                   Query Match
Best Local
                                                                                                                                                                       SEQ ID NO 149
                                                         Matches
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 149
SOFTWARE: Patentin Ver. 2.
                                                                                                                                                        LENGTH: 697
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                                                                  Similarity
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
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73.0%;
                                              Score 2576.5; DB 11; Length Pred. No. 8.2e-195; 1; Mismatches 2; Indels 1
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RESULT 3 ,
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       Query Match
Best Local Similarity
Matches 452; Conserv
                                                                                                                                                                                                                                                                        Sequence 8, Application US/09910600 Publication No. US20030036631A1 GENERAL INFORMATION:
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                                                                                                              SEQ ID NO 8
                                                                                                                     CURRENT APPLICATION NUMBER: US/09/910,600 CURRENT FILING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/220,139 PRIOR FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                               APPLICANT: Longphre, Malinda
APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES
                                                                                                                                                                                                          FILE REFERENCE: D0003NP
                                                                   LENGTH: 544
TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
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APPLICANT: Baker Kevin P
APPLICANT: Botstein, Dav.
APPLICANT: Desnoyers, Lu
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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Botstein, David
Desnoyers, Luc
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Ferrara, Napoleon
Filvaroff, Ellen
                             Paoni, Nicholas F.
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ton, David L.
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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DR APPLICATION NUMBER: 60/079656

DR FILING DATE: 1998-03-26

DR APPLICATION NUMBER: 60/079664
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DR FILING DATE: 1997-11-03
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
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DR FILING DATE: 1998-05-13
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                                                                                                                    GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP
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NQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK
                                                                 KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
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DR FILING DATE: 1998-04-22

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DR FILING DATE: 1998-04-22

DR APPLICATION NUMBER: 60/082700

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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
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FILING DATE: 1998-04-09
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60/081817 60/081955 60/081229 60/081203

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APPLICATION NUMBER: 60/081195 FILING DATE: 1998-04-08

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OR APPLICATION NUMBER: 60/084637
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APPLICATION NUMBER: 60/ FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-04-23

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CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-10-13

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Shelton; David L.
Stewart, Timothy A.
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Gurney, Austin L.
Hillan, Kenneth J
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Wood, William I.
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OR APPLICATION NUMBER: 60/082796

OR APPLICATION NUMBER: 60/083336

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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081070
FILING DATE: 1998-04-08
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/081229
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                                                      FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV 120
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APPLICANT: Williams, r. micholand Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630p1C9
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Botstein, David
Desnoyers, Luc
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                                                                                                                                                                                           Pan,
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                                                                                                                                                                                                           Napier, Mary A.
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Sophia S.
                                                                                                                                                                                             James;
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APPLICATION NUMBER: 60/085704
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                        FQ 512
                                                                                                                                                                                                                          NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                                                                                                              LVISISRDNTPD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                           NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE
                                                                                                                                                                                                                                                             WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
                                                                                                                                                                                                                                                                                                                LVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHP
                                                                                                                                                                                                                                                                                                                                                                                 TGAALSSQGTKPTTSHESVLSETPRPQDHDTDLTCHVDESRKGVSAQRTVRLRVAYAPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                   -----VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Pred. No. 2.3e
1; Mismatches
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2.3e-170;
nes 3;
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RESULT 7 US-09-999-832A-259

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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR FILING DATE: 1998-03-11
PRIOR PRIOR DATE: 1998-03-11
PRIOR PPLICATION NUMBER: 60/077649
PRIOR PPLICATION NUMBER: 60/07791
PRIOR PPLICATION NUMBER: 60/078004
PRIOR PILING DATE: 1998-03-12
PRIOR PPLICATION NUMBER: 60/078086
PRIOR PPLICATION NUMBER: 60/078886
PRIOR PPLICATION NUMBER: 60/078886
PRIOR PPLICATION NUMBER: 60/078936
PRIOR PILING DATE: 1998-03-20
PRIOR PPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078939
PRIOR PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR PRICOR DATE: 1998-03-20
PRIOR PRICOR DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/066364 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: 60/077450 PRIOR FILING DATE: 1998-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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APPLICATION NUMBER: FILING DATE: 1998-03
                                             APPLICATION NUMBER: FILING DATE: 1998-03
                                                                                      APPLICATION NUMBER: FILING DATE: 1998-03
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Grimey, Austin L.
Grimey, Wonneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy, Margaret Ann
Shelton, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paoni,
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09999832A o. US20020192706A1
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Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        James;
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NUMBER: 60/079664
1998-03-27
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                                           1998-03-26
                                                                                        1998-03-25
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                                                                 60/079656
                                                                                                            60/079294
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APPLICATION NUMBER: 60/079663 FILING DATE: 1998-03-27

1998-03-

60/079728

PRIOR

1998-03-3

60/080327

60/080194

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APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:

1998-03-

60/080105 60/079923

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R APPLICATION NUMBER: 60,
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60,
R FILING DATE: 1998-05-13
R APPLICATION NUMBER: 60,
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R APPLICATION NUMBER: (
R FILING DATE: 1998-05
R APPLICATION NUMBER: (
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R APPLICATION NUMBER: (
R FILING DATE: 1998-05
R APPLICATION NUMBER:
                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/085704
PTILING DATE: 1998-05-15
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 1998-09 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 1998-0: APPLICATION NUMBER:
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FILING DATE: 1998-04-
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                                     121
              181
                                                            121
                                                                                   61
                                                                                                                                                                                    450;
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                                                                                                                                 Similarity
TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
                                                                                               FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                                   ERGSYVRYNEMNDGFFLKVTALTQKPDVYIPETLEPGQPVTVICVENWAFEECPPPSFSW
                                                                                   FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVIRDAQMQDESQYFFRV
                                   ERGSYVTYNFMNDGFFLKVT----
                                                                                                                                                                                   Conservative
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1: 1998-04-29
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74.8%;
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                                                                                                                                                                                 Score 2265; DB 10;
Pred. No. 2.3e-170;
1; Mismatches 3;
                                                                                                                                                                                                       Length
                                                                                                                                                                                 Indels 148;
                                                                                                                                                                                                          544;
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DR APPLICATION NUMBER: 60/081819
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081952
DR FILING DATE: 1998-04-15
DR APPLICATION NUMBER: 60/081838
DR FILING DATE: 1998-04-15

APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817

APPLICATION NUMBER: 60/1 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/1 FILING DATE: 1998-04-09

60/081229

60/081203

APPLICATION NUMBER:

1998-04-15

FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08

60/081195

FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081071 FILING DATE: 1998-04-08

APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-01 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60 FILING DATE: 1998-03-3 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 FILING DATE: 1998-03-3:

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60/082796 60/082797 APPLICATION NUMBER: 60
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60/082700 60/082804 60/082704

APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
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APPLICANT: Baker Kevin P
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Wood, William
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Desnoyers, Luc
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RAPPLICATION NUMBER: 60/079664

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APPLICATION NUMBER: 60/077791
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Pred. No. 2.3e-170;
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Best Local Similarity
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LENGTH: 544
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391 KRRTQTETPRPRFSRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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Pred. No. 2.3e-170;
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                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/978,585A CURRENT FILING DATE: 2001-10-16
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ERGSYVTYNEMNDGFFLKVT---
                                                                                                  MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYW
                                               FKAVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAKGNCSLVTRDAQMQDESQYFFRV
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Gao, Wei-Qiang
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D. US20030049633A1
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Pred. No. 2.3e-170;
1; Mismatches 3;
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PRIOR ELICATION NUMBER: 60/062250	CURRENT AFFILICATION NUMBER: US/US/J/6/151A CURRENT FILING DATE: 20/0-10-10 DUTON ADDITARTON NUMBER: 00/0-10-66	FILE REFERENCE: FOR SOME AND	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	APPLICANT: Williams, P. Mickey APPLICANT: Wood, William I.	APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel		Paon	APPLICANT: Napter, Mary A. APPLICANT: Pan, James;	Kuo,	APPLICANT: Hillan, Kenneth J APPLICANT: Kljavin, Ivar J.	Gurney, Austi	Godowski	APPLICANT: Gerritsen, Mary E. APPLICANT: Goddard, Audrey	Gerber, Hai	APPLICANT: Gao. Wei-cland		Eaton, Da	APPLICANT: BOTSTEIN, DAVIG	Baker Kevi	GENERAL INFORMATION: APPLICANT: Ashkenazi. Avi	Publication No. US20030050239A1	978-191A-	RESULT 11	543 EQ 544	= :	511 FO 512	483 NOKKOYOLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 542	451 NOKKOYOLPSFPEPKSSTQAPESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVK 510	423 KRRTQTETPRPRESRHSTILDYINVPTAGPLAQKRNQKATPNSPRTPPPPGAPSPESKK 482	391 KRRTQTETPRPRESRHSTILDYINVVPTAGPLAQKRNQKATPNSPRTPLPPGAPSPESKK 450	363 GEFTCHARHPLGSQHYSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILP 422	331 GEFTCHARHPLGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIINKILP 390	303 NIGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 362	271 NLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHE 330	243 WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE 302					FAT
PRIOR FILING DATE: 1998-04-09 PRIOR APPLICATION UNMBER: 60/081229 PRIOR FILING DATE: 1998-04-09	APPLICATION N	APPLICATION N	APPLICATION N	APPLICATION N	; PRIOR APPLICATION NUMBER: 60/081070; PRIOR FILING DATE: 1998-04-08	FILING DATE: 1998-04-0	FILING DATE: 1998-0	; PRIOR FILING DATE: 1998-04-01 ; PRIOR APPLICATION NUMBER: 60/080333	AP	ΑP	FILING DATE: 1998-0:	FILING DATE: 1998-0:	; PRIOR FILING DATE: 1998-03-31	PPLICATION NUMBER: 6	APPLICATION N	; PRIOR FILING DATE: 1998-03-30	FILING DATE: 1998-0:	FILING DATE: 1998-0: APPLICATION NUMBER:	A G	Ę Ą	; PRIOR APPLICATION NUMBER: 60/079663 ; PRIOR FILING DATE: 1998-03-27	FILING DATE: 1998-0	FILING DATE: 1998-0:	FILING DATE: 1998-0: APPLICATION NUMBER:	APPLICATION NUMBER: 6	₽P	ΞP	FILING DATE: 1998-03	FILING DATE: 1998-0:	FILING DATE: 1998-03	FILING DATE: 1998-0	FILING DATE: 1998-0:	FILING DATE: 1998-03	FILING DATE: 1998-0: APPLICATION NUMBER:	FILING DATE: 1998-0: APPLICATION NUMBER:	FILING DATE: 1998-0: APPLICATION NUMBER:	FILING DATE: 1997-1: APPLICATION NUMBER:	<pre>; PRIOR FILING DATE: 1997-11-13 ; PRIOR APPLICATION NUMBER: 60/066364</pre>	AP	TRICK FILING DATE: 199/-11-03

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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
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PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
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PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR APPLICATION NUMBER: 60/083326
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PRIOR APPLICATION NUMBER: 60/083495
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OR APPLICATION NUMBER: 60/081838
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OR APPLICATION NUMBER: 60/085689
OR FILING DATE: 1998-05-15
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Sequence 259, Application US/09978403A Publication No. US20030050240A1 GENERAL INFORMATION:

APPLICANT: Ashkenazi, APPLICANT: Baker Kev

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APPLICANT: Tumas, Daniel
APPLICANT: Walliams, P. Mickey
APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucl
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
FILE REFERENCE: P2530P1C17

PRIOR FILLING DATE: D2020319
PRIOR PRIOR PRILICATION NUMBER: 020406230
PRIOR FILLING DATE: 1909-11-103
PRIOR APPLICATION NUMBER: 050/06230
PRIOR PRILING DATE: 1909-11-113
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PRIOR APPLICATION NUMBER: 050/077450
PRIOR APPLICATION NUMBER: 050/077450
PRIOR APPLICATION NUMBER: 050/077450
PRIOR APPLICATION NUMBER: 050/077641
PRIOR APPLICATION NUMBER: 050/078004
PRIOR FILLING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 050/078066
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Desnoyers, Luc
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f, Ellen
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OR FILING DATE: 1998-04-15
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OR APPLICATION NUMBER: 60/081070
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
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APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/085700
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APPLICATION NUMBER: 60/084639
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                                          LVISISRDNTPD----
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                                                                                     TGAALSSQGTKPTTSHFSVLSFTPRPQDHDTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD 240
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                                                                  -VLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRD
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Pred. No. 2.3e-170;
1; Mismatches 3;
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CURRENT APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi, Avi
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Shelton, David L.
Stewart, Timothy A.
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Kuo, Sophia S.
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Desnoyers, Luc
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10
PRIOR PELICATION NUMBER: 60/077641
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RESULT 14
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; Sequence 259, Application US/09999833A
~~~11cation No. US20030054405A1
      Publication No. US2003005440
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eston, Dan
APPLICANT: Firvaroff, Elle
APPLICANT: Filvaroff, Elle
APPLICANT: Filvaroff, Elle
APPLICANT: Gao, Wei-Qiang
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
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Botstein, David
Desnoyers, Luc
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                      Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
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      Wei-Qiang
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pred. No. 2.3e-170;
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CURRENT ETLING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR PRIOR PRIOR NUMBER: 60/063311
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/06364
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
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OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/080105
OR FILING DATE: 1998-03-31
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FILING DATE: 1998-03-27
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
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Williams, P. Mickey
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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                                        WGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLE
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1; Mismatches 3;
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APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15

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R FILING DATE: 1998-04-21
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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Baker Kevin P.
Botstein, David
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Wood, William I
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Tumas, Daniel
Tumas, P. Mickey
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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Margaret Ann
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APPLICATION NUMBER: 60/081952
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-DB-GenEmb1 -QFMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
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SUMMARIES

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ALIGNMENTS

RESULT 1

ОУ ,	Qу :	Qy Db 2:	US-09-937-636-3	Query Match: DB:	Percent Similarity: Best Local Similarity:	Pred. No.:	,	BASE COUNT									CDS	gene		source	FEATURES			MEDLINE		RS		ORGANISM	KEYWORDS SOURCE	ACCESSION	LOCUS	AF311905
41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20	36-3 (1-512) x AF311905 (1-3124)	96.648	84.39% Conservative:	Length:		QEELHYATLNEPGVRPRPEARWPKGTQADYAEVKFQ" 769 a 910 c 813 g 632 t	AGPLAQKRNQKATPNSPRTPLSPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQES	TQRQQVLSPSQPSDPGVLELPRVQVEHBGEFTCHARHPLGSQHVSLSLSVHYKKGLIS	ALDS CAPACIANT SHARK WITH THE COLOR TO THE CHARGE OF THE C	TVICVENWAREECPPESFSWIGAALSSOCITESHESVLSFTPRPODHNTDLTCHVD FCBKCVCVCVDETVBI VAXVADDIQ VICTORDANDA TEDODOCANIEV TEALANDOCATE TO	VPRODUTGSTPAYGYNEKAVTETTKGAPVATUHQSREVENSTRGREDITTEDOAKGNCS IVITADAOMODESOVETEBVERGSVYKBVATUHQSREVENSTRGREDITTEDOAKGNCS LUTTDAOMODESOVETEBVERGSVYKBVATUHQSREVENSTRGREDITTEDOAKGNCS	/db_xref="GI:15217163". /db_xref="GI:15217163". /tranglation="WII.DIII.SGII.GGGOAMDGDEWIDVORGIMYDRGIOTGVDOGGG	/product="gialic acid-binding Ig-like lectin 10" /protein id="aak07547 1"	/note="Siglec-10; similar to other siglec family members"	223 2031	13124 /geno="STGTEC10"	/mol_type="mRNA" /db xref="taxon:9606"		Xiangyin R fiers	Direct Submission Direct Submission Submitted (15-AUG-2001) Department of Immunology, Second Military	2 (bases 1 to 3124)	J. BIOI. CREM. 2/6 (30), 28106-28112 (2001) 21359381 11358961	Cloning and characterization of Siglec-10, a novel sialic acid binding member of the Ig superfamily, from human dendritic cells	Li,N., Zhang,W., Wan,T., Zhang,J., Chen,T., Yu,Y., Wang,J. and Cao,X.	Manmalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3124)	ns Metayoa: Chordata: Craniata: Vortobrata:	S	AF311905 1 GT-15217165	AF311905 3124 bp mRNA linear PRI 21-AUG-2001 Homo sapilens sialic acid-binding Ig-like lectin 10 (SIGLEC10) mRNA,	
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Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Store: Stor	AX365530 LOCUS LOCUS AX365530 LOCUS LOCUS AX365530 LOCUS SETNITION Sequence 15 from Patent WO0208257. ACCESSION AX365530 VERSTON AX365530 KEYWORDS SOURCE ORGANISH Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. AUTHORS AUTHORS LOngphre,M., Chang,H. and Whitney,G. AUTHORS Novel siglecs and uses thereof; Novel siglecs Nove	1483 351 1543 371 1603 391 1663 411 1723 1783 431 1783 451 1843 471 1903	331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu
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Yan,W.P. and Longphre,M.
A new Siglec family member, SIGLEC10, is expressed
immune system and has signaling properties similar
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  PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg
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Dundee, Dow Street, Dundee DD6 8AT, Scotland, United Kingdom
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CCe BH CCh: SCOI 11.1milla 11.2 SCOI 11.2 STOI	LOCUS DEFINITION Sequence 1 from Pate ACCESSION AX365516 VERSION AX365516.1 GI:18697 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Eukaryota; Metazoa; Mammalia; Eutheria; AUTHORS LOngphre, M., Chang, H TITLE TOURNAL Patent: WO 0208257-A
BRISTOL-WEEKS SQUIEM COMPANY (US): Location/Qualifiers 1.2655 2.265 // Organism="Romo sapiens" // Moltype="alonnic DMA" /	ONA eta; Ve chini;
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                                               AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla
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                                                                                                                                             AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla
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Gurney,A.L., Pan,J.,
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                                ATCGGCATCACGGCTCTTCTTTTCCTCTGCCTGGCCCTGATCATCATGAAGATTCTACCG
                                       IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
E 1 (bases 1 to 3099)
S Kikly, K.K. and Miller, C.L.E.
Sialoadhesin family 4(SAF-4) cDNA
Patent: JP 2001502359-A 1 20-FEB-2001;
SMITHKLINE BEECHAM CORP
OS Homo sapiens (human)
PN JP 2001502359-A/1
PD 20-FEB-2001
PD 20-FEB-2001
PD 20-FEB-2001
PR 27-MAY-1997 US 60/047572
PR 27-MAY-1998 JP 1999500864
PR 27-MAY-1997 US 60/047572
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/db_xref="taxon:9606"
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DB 470 181 ThrolyAlaAlaLeuserserdinglythriysProThirthrSerHisPheserValLeu 471 471 472 201 SerPherithrokrgerodinaspHisAsphrAsphearthrySHisPyAlaspheser 787 1811	470 161	Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 	Incluince Acceptance Incluince Inc	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	51 AIGCIACIGCCACIGCIGCIGCIGCIGCIGCIGGGGGGGG	-09-937-636-3 (1-512) x HDULL517 (1-3099) 1 MetLeuLeuFroLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg	64.85% MISMATCHES: 82.06% Indels: 6 Gaps:	Pred. No.: 1.11e-120 Length: 3099 Score: 2220.50 Matches: 452 Percent Similarity: 64.998 Conservative: 1		ASE COUNT 769 a 908 c 813 g 607 t 2 others	urce	FH Key Location/Qualifiers FT source 1. 3099 FT /Organism='Homo sapiens (human)'. FFATURES Location/Qualifiers	A61K39/00, A61K39/395, A61K48/00, C07H21/04, C07K14/435, C07K14/705, PC C07K16/00, PC C07K16/00, C07K16/00, C07K16/01, C12N15/01, C12N15/11, C12N15/12, C12N15/63 CC	PN 3F 2001302337-A/2 PD 20-FEBB-2001 PF 27-MAY-1998 JP 1999500864 PR 27-MAY-1997 US 60/047572 PR 27-MAY-1997 US 60/047572	JOURNAL Patent: JP 2001502359-A 2 20-FEB-2001; SMITHKLINE BEECHAM CORP COMMENT OS Homo sapiens (human)	Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. REFERENCE 1 (bases 1 to 3099) AUTHORS Kikly,K.K. and Miller,C.L.E. TITTE Stalpadheein family A/SAF-A/CDNA	;hordata; Craniata; Vertebrata; F
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Kitzig,Fr., Martinez-Barriocanal,A., Lopez-Botet,M. and Sayos,J.
Cloning of two new splice variants of Siglec-10 and mapping of
interaction between Siglec-10 and SHP-1
Blochem. Blophys. Res. Commun. 296, 355-362 (2002)
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Homo sapiens stalic acid-binding pa
(Siglec-10 Sv3) mRNA, complete cds.
AY032685
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Kitzig,F., Alvarez-Errico,D., Sayos,J. and Lopez-Botet,M.
Direct Submission
Submitted (17-APR-2001) Immunology, Universitat Pompeu Fabra
(CEXS), Dr. Aiguader No. 80, Barcelona 08003, Spain
                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 2 (bases 1 to 2126)
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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(1-2126)φ Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2126 448 1 5 243

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3 SerValProCysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr [1]	#W11type=genoments but Alignment Scores: Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match: Ouery Matches: Ouery Matche	aniata; Vertebrata; Euteleostom tarrhini; Hominidae; Homo. y,G. 02;	Qy 436 ArgThrProLeuProProGlyAlaProSerProGluSerLysLysAsnGlnLysLysGln 455

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1149 GAGGGTCTGCACTGCAGCTGCTCCCAGGCCAGCCCGGCCCCTCTCTGCGCTGGTGG 1208 354		969 GTTCTGAGCCCCTCCAGCCCTCAGACCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTG 1028 328 GluHisGluglyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSer 347	288 LeuValCysValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGln 307	789 CTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTTGATTGCCAAGCAAACAGGACA 848 268 ValleuGluAsnLeuGlyAsnGlyThrSerLeuProValleuGluGlyGlnSerLeuCys 287 + - - - - - - - - - - - -	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267	1 61	TCCCATCCCTGGGGCCCTAGACCCCCTGGGGCCTGGAGCTGCCCGGGGTGAAGGCTGGGGAT		252 252 549 CAGGGAAATGTCCCATACCTGGAAGCCCAAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCT 608	238 ProArgAspLeuValIleSerIleSerArgAspAsnThrProAsp 252	218 AspPheSerArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAla 237	8 ServalLeuSerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisVal	PheSerTrpThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerH1sPhe	158 GlnProValThrValTleCysValPheAsnTrpAlaPheGluGluCysProProSer 177	303 TTTCGGGTGGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT
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Qy 163 IleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrpThrGly 182	Db 72 ACTCAGAAGCCTGATGTCTACATCCCCGAGACCCTGGAGCCCGGGCAGCCGGTGACGGTC 131	Qy 143 ThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProValThrVal 162	Qy 123 GLySerTyrValargTyrasnkneMetAsnasputykneknekelollySvaltniralaled 142	-09-937-636-3 (1-512) x AX365518 (1-2823)	7 Match: 71.30%	9.69e-104 Length: 1929.50 Matches: ilarity: 67.488 Conservative: Similarity: 67.308 Mismatches:	677 a	source	TITLE Novel siglecs and uses thereof JOURNAL Patent: WO 0308257-A 3 31-JAN-2002; BRISTOL-MYERS SQUIBS COMPANY (US) FEATURES LOCATION/QUALIFIERS FEATURES	;	VERSION AX365518.1 GI:18697087 KEYWORDS . SOURCE Homo sapiens (human) ORGANISM Homo sapiens	AX365518 AX365518 AX365518 DEFINITION Sequence 3 from Patent WO0208257. ACCESSION AX365518	QY 3/1 116GIY.1ETRIALEULEULPELPELEULYSLEURIALEULTELE 353	351 ServalHisTyrLysuysGlyLeulleserTurAlapheserAsno	1844 GGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCAGCCTC	1784 CCCTCCAGCCCTCAGACCCCCGGGGTCCTGGAGCTGCCTCGGGTTCAAGTGGAGCACGAA	291 1724	2/1 ASTLEUGLYASINGLYTINTSETLEUFTOVALLEUGLUGLYGINGETLEUGYSLEUWAICYS	253ProprogluasnLeuargValMetValSerGlnalaasnArgThrValLeuGlu

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Qy 466 rSerThrGl	21 ArqivsGlvVəlSerAləqlnArqThrVəlArqienArqVəlAləTvrAləDroArqAso	9
Db 1725TCCAT	AGCTTCACGCCCAGGACCCCAGGACCACAACAACAACAACAACAA	D :
Qy 452 nLysLysGl	01 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCvsHisValAspDheSer 2	φ
Db 1676 CCTCAGGCT	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200 	Db Qy
1632	609 ACGGTCATCTGTGTGTTTAACTGGGCCTTTGAGGAATGTCCACCCCCTTCTTTCT	ДЬ
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<u> </u>	61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	P 64
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AX365519.1 GI:18697088 Homo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 Longphre,M., Chang,H. and Whit Novel siglecs and uses thereof Patent: WO 0208257-A 4 31-JAN- BRISTOL-MYERS SQUIBB COMPANY (Location/Qualifiers 1. 1665 /organism="Homo sapie /mol_type="genomic DN /db_xref="taxon:9606"	07 aGluValLysphe 511 37 TGAGGTCAAGTTC 1949 AX365519 1665 bp	496GlnAlaArgMetProLysGlyThrGlnAlaAspTyrAl 507 ::: :::	478 uGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu 495 :::	466 rSerThrGln	452 nLysLysGlnTyrGlnLeuProSerPheProGluProLysSe 466	441 ProGlyAlaProSerProGlu-SerLysLysAsnGl 452 1676 CCTCAGGCTCCGCTGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGA	422 LeuAlaGlnLysArgAsnGlnLysAlaThrProAsnSerProArgThrProLeuPro 440	403 PheSerArgHisSerThrIleLeuAspTyrIleAsnValValProThrAlaGlyPro 421 ::::::	391 LysArgArgThrGlnThrGluThrProArgPro	371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390	351 SerValHisTyrLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370	331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350 	311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330

Db	Qy	Дb	Qy	망	Qy	Db	Qy	В	Qy	Db	Qy	망	Qy
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Search completed: October 8, 2003, 21:48:29 Job time : 5749 secs

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Command line parameters:

MODEL-frame+_p2n.model -DEV=x1h
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-DB-N_Geneseq_19Jun03 -QFMT-fastap -SUFFIX-P2n.rng -MINMATCH-0.1 -LOOPCL-0
-LOOPEXY=0 -UNITS-bits -START=1 -END=-1 -MATIX-biosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_HIN-0 -ALIGN-15
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-NO_MMAP -LARGEQUERY -NEG_SCORES-0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
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Ygapop 10.0 , Ygapext
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Pred. score No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed,

> and is derived by analysis of the total score distribution.

SUMMARIES

No t	Score	% Query Match	Length	DB	ID	Description
- :	70	100.0	53	- i	AAA37847	n obesity pro
N	0		20	24	4336	encoding sia
. w	580.	٠.	02	2 2	X433	encoding sial
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ALIGNMENTS

RESULT 1
AAA37847
ID AAA37847
XX AAA37847
AC AAA3
XX AAA3
XX Huma
XX Huma
KW Huma
KW Obee
XX Obe
XX Y
FT CDS AAA37847; AAA37847 standard; DNA; 1536 BP. 12-FEB-2001 (first entry) 1 officiation

Human obesity protein binding protein-2 homologue coding sequence #1.

Human obesity protein binding protein-2 homologue; hOB-BP2h; obesity; obesity-related disorder; therapy; ds.

Homo sapiens Location/Qualifiers
1..1536

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Alignment Scores:
pred. No.:
Score:
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                                                                                                                                                                                                                                                                                                      This sequence encodes a human obesity protein binding protein-2 homologue (hOB-BP2h) of the invention. The hOB-BP2h nucleic acids and polypeptides may be used for the manufacture of a medicament for the treatment of obesity and/or obesity-related disorders. The hOB-BP2h nucleic acids are useful as probes or amplification primers in the detection, quantification or isolation of gene sequences or transcripts, for recombinant expression of hOB-BP2h polypeptides, as immunogens in the preparation and screening of antibodies, and in sense or antisense suppression of one or more hOB-BP2h genes or nucleic acids, host cell or tissue in vivo or in vitro. Antigenic epitope-bearing peptides and polypeptides are useful for raising or screening antibodies that specifically binds to the hOB-BP2h polypeptides.
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               CysSerLeuValIleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal
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                                                         ProGlyAlaProSerProGluSerLysLysAsnGlnLysLysGlnTyrGlnLeuProSer
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                                                                                    CC related lectin) protesn (I). Pharmaceutical compositions comprising (I)
CC are useful for treating immune system diseases such as asthma, leukaemia
CC or other allergic or inflammatory diseases. Extracellular domains of (I)
CC represent potential markers for screening, diagnosis, prognosis,
CC follow-up assays, and imaging methods. (I) is useful as a target for
CC drugs which inhibit inflammation, tissue damage and remodeling in
CC osteoarthritis, Crohn's diseases such as allergic rhinitis,
CC osteoarthritis, etc. (I) is also useful for monitoring the course of
CC disease or disorders, and for identifying agents that bind with and/or
CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis
CC methods, and to detect the presence and/or amount of SIGLEC-BMS
CC (II) are useful as nucleic acid probes are useful for screening genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein molecules useful for treating immune system diseases such as asthma, leukaemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease
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CC drigs which inhibit inflammation, tissue damage and remodeling in CC asthma; and inflammatory disease, psoriasis, rheumatoid arthritis, CC osteoarthritis, Crohn's disease, psoriasis, rheumatoid arthritis, CC osteoarthritis, etc. (I) is also useful for monitoring the course of CC conjunctivitis, etc. (I) is also useful for monitoring the course of CC disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid CC molecules (II) encoding (I) are useful in diagnosis and/or prognosis CC nucleotide sequences and/or SIGLEC-BMS proteins in a biological sample. CC (II) are useful as nucleic acid probes are useful for screening genomic clibrary to isolate a genomic clone of SIGLEC gene. SIGLEC-BMS gene copy commber is determined for detecting diseases or disorders associated with CSIGLEC-BMS transcripts or proteins. The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells expressing SIGLEC-BMS proteins cand in diagnostic imaging technology. ABK43360-ABK43411 represent when a signal content of the invention. The invention relates to an isolated SIGLEC (sialic acid-binding Igrelated lectin) protein (I). Pharmaceutical compositions comprising are useful for treating immune system diseases such as asthma, leukas or other allergic or inflammatory diseases. Extracellular domains of represent potential markers for screening, diagnosis, prognosis, follow-up assays, and imaging methods. (I) is useful as a target for ins of (I) acid

Sequence BP; 699 Α, 933 Ç; 790 ç; 602 T; 0 other;

Query Match:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
95.36%	73.17%	73.31%	2580.50	5.94e-176	
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253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	1089 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTGTG 1148	252 252	1029 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 1088	252 252	969 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCCTCCTCGTCCCATCCC 1028	252 252	909 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC 968	252 252	849 CTTGTTATCAGCATTTCACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGAAAT 908	241 LeuVallleSerlleSerArgAspAsnThrProAsp 252	221 ArgLyselyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 21 ArgLyselyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 21 ArgLyselyValSerAlaGlnArgGACGTCGTCGACTCCGTGTGGCCTPATGCCCCCAGAGC 848 289 AGAAAGGGTGTGACGCAAGAGGACGTCCGACTCCGTGTGGCCTPATGCCCCCAGAGAC 848	729 AGCTTCACGCCCAGACCCCAGGACCACAACACCGACCTCACCTGCCATGTGGACTTCTCC 788	201 SerPheThrProArgProGlnAspH1sAspThrAspLeuThrCysH1sValAspPheSer 220	69 ACGGGGGCTGCCCTCCCCAAGGAACCAACGACCTCCCACTTCTCAGTGCTC 7	81 ThrGlvAlaAlaLeuSerSerGlnGlvThrLvsDroThrThrSerHisPheSerValleu 20	101 THIVALLILECYSVALPHEASHTIPALBPHEESIUGLUCYSPIOPIOPIOSEIPHESETTIP 180		141 AlaLeuThrGintysProAspValTyrIleProGitOThrCeuGiuProGlyGinProVal 160 	89 GAGAGAGGAAGCTATGTGAGATATAATTTCATGAACGATGGGTTCTTTCT	21 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 14	TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTC	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	369 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 428	81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100	309 TTCAAAGCAGTGACTGAGACAACGAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 368	eLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg		41 CysSerPheSerTyrProArgGlnAspTrpThrGlvSerThrProAlaTyrGlvTyrTrp 60	TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 2	21 PheTrnTleAraValGlnGlnSarValMetValDrnGlnGlvIenGvsTleSerValDrn 40	1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20	37-636-3 (1-512) x ABK43373 (1-3024)	24 Gaps: 2
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                                                                                                                                                  represent potential markers for screening, diagnosis, prognosis, follow-up assays, and imaging methods. (I) is useful as a target for drugs which inhibit inflammation, tissue damage and remodeling in asthma, and inflammatory diseases such as allergic rhinitis, controlled the course of asthma, and inflammatory diseases such as allergic rhinitis, controlled the course of conjunctivitis, etc. (I) is also useful for monitoring the course of disease or disorders, and for identifying agents that bind with and/or modulate the biological activity of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are useful in diagnosis and/or prognosis methods, and to detect the presence and/or amount of SIGLEC-BMS nucleic acid probes are useful for screening genomic clibrary to isolate a genomic clone of SIGLEC-Gene SIGLEC-BMS gene copy number is determined for detecting diseases or disorders associated with SIGLEC-BMS transcripts or proteins. The SIGLEC-BMS proteins and in diagnostic imaging technology. ABK43360-ABK43411 represent changing technology. ABK43360-ABK43411 represent
                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated SIGLEC (sialic acid-binding Ig-
related lectin) protein (I). Pharmaceutical compositions comprising (I)
are useful for treating immune system diseases such as asthma, leukaemia
or other allergic or inflammatory diseases. Extracellular domains of (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated SIGLEC (sialic molecules useful for treating leukaemia, allergic rhinitis,
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system disease; leukaemia; allergy; inflammatory disease;
damage; allergic rhinitis; osteoarthritis; Crohn's disease;
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{\tt MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg}
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Local Similarity:
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2000WO-US00277.
2000WO-US00376.
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Goddard
Kljavin
Shelton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78997 represent PCR primers and probes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel PRO polypeptides and polynucleotides to target bloactive molecules to specific cellular activities -
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Kuo SS, Nap
Stewart TA,
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PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; coladrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorders.
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                                                                          02-JUL-2002;
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431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys 450	SALA 4	Hyshighty incomes a control of the c	1 ITEGATY TETTIA ALGULEUR PRECENS PROCESSES ATCACCATO CONTROL OF THE CONTROL OF T	51 92	GlyGluPheThrCysHisAlaArgHisProLeuGlySerGliHisValseLieuseLieu	11 ProSerGlnProSerAspProGlyValLeuGluLeuProAspValGlnValGluHisGlu	 (4)	71 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 2	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270 	252	2. ACACACAMAN TURBARA TARABAN BARARA TARABAN SA	.52	12 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 77	552 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGACAGC 711	52	241 LeuVall1eSerIleSerArgAspAsnThrProAsp	21 ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220 	66	81 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSer	165 465

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Pan Baker KP, Smith Chen J, nith V, W , Desnoyers L, Goddard A, Go Watanabe CK, Wood WI, Zhang Godowski PJ, ang Z; Gurney AL

2003-332039/31. ABU67464.

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification -

Claim 2; Fig 117; 706pp; English.

CC transmembrane (PRO) polypeptides. Also disclosed is an antibody that consenbrane (PRO) polypeptides, a method for stimulating the crelease of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the cells with a PRO polypeptide, a method for stimulating the cells with a PRO polypeptide, a method for detecting the presence of a cumour in a mammal and an oligonucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in clintomosome and gene mapping, in generating antisense RNA and DNA, in clintomosome and gene mapping, in generating antisense RNA and DNA, in clintomosome and gene mapping, in generating antisense RNA and DNA, in consorme identification, as chromosome markers protes, for chromosome identification, as chromosome markers, as therapeutic agents for stimulating the release of TNF-alpha from human blood, for coids may also be used diagnostically for tissue typing. The sequences of presented in AcAO5700-ACAO60004 are the cDNAs encoding the PRO propertides and invention of chondrocytes and inventions. invention of the invention. discloses human nucleic acids encoding secreted g secreted and an antibody that

689 Α. 798 Ç 717 ç; 560 Τ, 0 other;

Pred. Score: Alignment Scores: Percent Similarity: No.: 2.54e-153 2265.00 74.92% Length: Matches: Conservative:

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(GETH) GENENTECH INC.

Ashkenazi A, Ferrara N, Goddard A, Kljavin IJ, Shelton DL, Ą A, Baker KP, I Filvaroff E, Godowski PJ, , Kuo SS, Napi , Stewart TA, Napier MA, IA, Tumas D, Botstein D, Desnoyers L, Eaton D; Fong S, Gao W, Gerber H, Gerritsen Grimaldi JC, Gurney AL, Hillan KJ; pier MA, Pan J, Paoni NF, Roy MA; Tumas D, Williams PM, Wood WI; ME;

WPI; 200 P-PSDB; 2003-288163/28. DB; ABU61110.

Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies .

Claim 2; Fig 92; 459pp; English.

The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The CC PRO polypeptides are useful for detecting other PRO polypeptides, for CC linking bloactive molecules to cells expressing PRO polypeptides, for CC linking bloactive molecules to cells expressing PRO polypeptides, CC for modulating biological activities of cells expressing PRO polypeptides, CC polypeptides, and for for identifying agonists or antagonists. The CC bloactive molecule maybe a toxin, radiolabel or antiopody, and causes CC polypeptides or death of the cell. The PRO polypeptides are useful for CC treating immune disorders, diabetes or hyper or hyper-insulinaemia, CC cardiac insufficiency, nervous system disorders, kidney disorders, CC bone and cartilage disorders or arthritis, tumours, and wound healing. CC The polynuclectide sequences encoding PRO polypeptides are useful as CC hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC generating transgenic animals or knockout animals, for the genetic CC analysis of individuals with genetic disorders, and in gene therapy. CC The present sequence data for this patent was obtained in electronic CC format directly from the USPTO web site at CC sequence data for this patent was obtained in electronic CC sequence and the USPTO web site at

Sequence P. 798 Ç <u>ن</u> 560 1 0 other;

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                                                        ss; cytostatic;
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                                         on; chondrocyte
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                                       chromosome mapping; gene mapping;
ecrosis factor-alpha; TNF-alpha; blood;
drocyte proliferation; tumour.
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Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	US-09-937-636-3 (1-512) x ABX97802 (1-2764) Oy 1 MetLeuLeuProLeuLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20	gnment Scores: 2.54e-153 Len d. No.: 2265.00 Mat cent Similarity: 74.92% Con t Local Similarity: 74.75% Mis ry Match: 83.70% Gap 25 Gap	PR 26-JUN-1998; 98US-090862P. PR 26-JUN-1998; 98US-09105P. PR 26-JUN-1998; 98US-091359P. PR 01-JUL-1998; 98US-0913544P. PR 01-JUL-1998; 98US-091478P. PR 02-JUL-1998; 98US-091628P. PR 02-JUL-1998; 98US-091628P. PR 02-JUL-1998; 98US-091632P. PR 02-JUL-1998; 98US-091632P. PR 02-JUL-1998; 98US-091632P. PR 10-AUG-1998; 98US-09598P. PR 11-AUG-1998; 98US-09589P. PR 26-AUG-1998; 98US-09599P. PR 26-AUG-1998; 98US-09599P. PR 26-AUG-1998; 98US-097952P. PR 26-AUG-1998; 98US-0997952P. PR 26-AUG-1998; 98US
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                                                                                                                                                                              AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160
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prostate tumour; rectal tumour; cervical tumour; liver tumour;
bone disorder; cartilage disorder; arthritis; sports injury.
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Search completed: October 8, 2003, 20:13:22 Job time : 459 secs

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-Q-/cgn2__l/USPTO_spool/US09937636/runat_08102003_083236_29976/app_query.fasta_1.711
-DB-EST -OFMT=fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-UTFMT=Dto -NORM-ext -HEAPSIZE-500 -MINLER-0 -MAXIEN-200000000
-USER-US09937638_@CGN.1_1_8810_@runat_08102003_083236_29976 -NCPU-6 -ICPU-3
-NO_MMAP -LARGEDUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1 AK042488 LOCUS DEFINITION

ORGANISM AK042488

2017 bp mRNA linear HTC 05-DEC-2002 mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630096C01 product:weakly similar to SIALIC ACID-BINDING LECTIN [Homo sapiens], full insert sequence.

AK042488 Mus musculus (house mouse) AK042488.1 GI:26335142 HTC; CAP trapper.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

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                                                                                             Adachi, T., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizune, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohoo, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Group Phase I & II Tem. CITE NAME OF COUNTY OF THE MOUSE TRANSCRIPTOME based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases I to 2017)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The
                                                                       Direct Submission
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Physical and Chemical Research
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FEATURES
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                                                                                                                                                                                                                                                                                              Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoham Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Encyclopedia Project of Genome Exploration Research Group in R
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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URL:http://fantom.gsc.riken.go.jp/.
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Please visit our web site for further details.
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome
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LysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArgGlu
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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/clone_lib="ROMO Sapiens PLACENTA COT 25-NORMALIZED"
/clone_"lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end cloned into the Not I and EcoR V
sites of the PCMVSPORT 6 vector. Library was normalized."
sites of the PCMVSPORT 6 vector. Library was normalized."
a 333 c 339 g 228 t 39 others
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	TITLE JOURNAL MEDLINE PUBMED PEFERENCE AUTHORS	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	RESULT 3 AK036698 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Qy Db	Фу	Qy Db
Sawa H. Sawa H. Bono, H. Bono, H. Bono, H. Bono, H. Bono, H. Boffelli, Gustin Stein, M.J Stein, M.H	Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 25 1076861 26 Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., RES., Kawai,J., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., RES., Kawai,J., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDMAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,		AK036698 Mus musculus adult male b library, clone:9830164H33 ACID-BINDING LECTIN [Hom AK036698 AK036698 1 GI:26331615 HTC; CAP trapper	300 uSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnPro 314	280 lLeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArgLe 300 :::	260 tValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuProVa 280 :::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Genter (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212, Eax:81-45-503-9216)
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Analysis of the mouse transcriptome based on of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3939)
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URL:http://fantom.gsc.riken.go.jp/.
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Please visit our web site for further
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                                                                                                                                                                                    /translation="MSLLLFILLSFILDGPOGOMESYVLQVQRIVKAQEGLCIFVPCSF
SSPEGKWLNRSPLYGVWFKGIRKPSLSFPVATMNKDKYLEWERAGRFQPLGDISKKNT
SLLIKDVOWGDSTNYFFRWERGFERFSFKEEERLQVEALTQKPDIFIFEVLEPGEFVT
VVCLFSWTFNOCPAPSFSWMGDAVSFQESRPHTSNYSVLSFIPGLQHHDTELTCQLDF
                                                                                                                                                                                                                                                                                                                                       /note="unnamed protein product; putative
weakly similar to SIALIC ACID-BINDING LECTIN [Homo
sapiens] (SPTR|Q96RL6, evidence: FASTY, 61.6%ID,
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/clone_lib="RIKEN full-length enriched mouse
/dev_stage="adult"
160._969
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/db_xref="GI:26331616"
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379 uCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGlnThrGlnThrPr 399	250	Qy
2414 10CCUCUQCUIICICCUUUUUUUUUUIIIIIIIIIIIIIII	2132 ATCTCTATGTCTATAACCATCTCTCTCTCTCTCTCTCATCCTTCATCCTCTGTTTCTCTG 2191	В
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3136 OICCIONACANCACANTA DE CONTRACTOR DE CON	2072 CTGTCTGTCTGTGTGTGTGTGTGTGTGTCTGTCTGTCTCTGTCTTTTGTGTCT 2131	οb
3152 CTTOCTGCAACACCACCCACACCACCACCACCTCCTCCTCCTCCTCC	. 250 250	Qγ
3605	2012 TGCTCCCTCTCCCTTATGTCTGTCTCTCTCTCTCTCTTTATCTATC	Дb
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35036	1952 TGGGGAGGGGGAAGGGGCAGGTTGGAACTCTTTTTACTGCTTCTCCCTACCCTCCATCT 2011	Дb
358 ulle	250 250	Qy
2972 CAACTGCTCCAGAGCCTGGCCTGCCCTCCCTGCGCTGGCGGCTGGGGGAGGGGCT	1892 TACGTTGGTCTCCTGGGGTCTTATAGGGCCGGTCCATTCCTTTTTGGGAAAATGAAAAGTC	D 5
357GlyLe 358	250	Q !
2912 CACAGACCCGCCCCAGATGTCCAGCCCCTCCTGCTCCTGGGAGGCCAAGGGTCTGCACTG	237 250 237 250 1833 CTTCTCCCAGATGCCCCCAGATCTCTTTCCTTATCAGCATGACAATGT-ATCAGG 1891	р. Q
356	1773 TTTCCCTGAGGGACTTCTCATGAGGAACAAAGCATTCCCCTCTGAAGTTGGCTCACAAAT 1832	DЪ
2852 TAGGCAAAAGGGACACTGGGGATCTGTGATGAGGGCCCAGCTGGTGACCATTCTCCTCCTC	236 236	Qy
255 01/00	1713 GGCGATGGTTGCTTCATTTCTGGTTGGTCTCGTGCCTTCTCTGGGATAGTGGTGCTTTTC 1772	DЬ
336 HISATAKAHISKICHENGLIYSETGIHTIN ATISELHENSELHENSELKOTGTGAGCTTGTGAG 2792 GTTGAGAGAGTGAGTTGAGTGAGCGATGTGAGCGTGTGAGCGTGTGAGCGTGTGAG	236 236	Qy
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Tissue Procurement: Invitrogen
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National Institutes of Health, Mammalian
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1 (bases 1 to 1099)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587803"
/lab_host="DH10B"
                                                        /note="Organ: Ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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              CAGCCCCCCTGCCCCGTTGAGCTTGGGTTCCTGCCAGGCAAAAAGTTCCTTCTCCTCCGA
                             rSerProProAlaArgLeuSer-TrpThr---GlnArgGlyGlnValLeuSerPro----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2385 row: d column: 06
High quality sequence stop: 685.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/
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5', mRA sequence.
BQ711946
BQ711946.1 GI:21850845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
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ValLeuGluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArg
                                             MetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuPro
                              ATGGTTTCCCAAGCAAACAGGACAGTCCTGGAAAACCTTGGGAACGGCACGTCTCCCCA
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                                                                                                                                                                                                                                                    /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2 EcoRI; cDNA made by oligo-dT priming. Directionally clone into EcoRI/XhoI sites using the following 5' adaptor: GCACCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a 304 c 244 g 151 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6215765"
                                                                                                                                                                                                                                                                                                                                                                                     /lab_host-"DH10B (phage-resistant)"
/clone_lib-"NIH_MGC_113"
                                                                                                                     2.97e-65
895.50
65.19%
64.85%
33.09%
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Primates;
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3 Homo
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CB554607
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithe Cercopithecinae; Macaca.

1 (bases 1 to 667)
Unpublished Contact: Holzman
                                                                                                                                Macaca mulatta (rhesus monkey)
Macaca mulatta
                                                                                                                                                             CB554607.1
EST.
                           Expressed sequence
                                                     Katze, M.G., Bumgarner, R.,
                                            Holzman,T.
                                                                                                                                                                                                                                                                             CCNTCCCCGGAATCCAAGAAGGAACCCGAAAAA
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                                                       Korth, M.,
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cDNA, mRNA sequence
                         macaque spleen
                                                       Feldman, R.,
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                                                       Amjadi, M.
                                                                                                                 Euteleostomi;
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Query Match
DB:
RESULT 7
HSM097253
ID HSM09
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                                              481
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University of Washington
Box 358070, Seattle, WA 91
Tel: 206 732 6156
Fax: 206 732 6055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ted@locke.hs.washington.edu
Similar to GenBank entry AF311905 AF311905
acid-binding Ig-like lectin 10 (SIGLEC10) m
8/2001
Plate: MMSP0040 row: D column: 05.
                                                                                                                                                                                                                                                                                                                  LysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla
                                            GluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgPro
                                                                                                                                                            CACGCTCAGCACCCGCTGGTGCTCTAGCACGTCTCTCTCAGCCTCTCCGTGCACTATAAG
                                                                                  GAGAGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCC
                                                                                                                       CAGCATCAGTTGCCCAGTTTCCCCAGAACCCCAAATGATCCACTCAAGCCCCAGAATCCCAG
                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                              (1-512)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Macaca mulatta"
/mol_type="mRNA"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="MMSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="monocytes"
/dev_stage="adult"
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824.50
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91.01%
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                                                                                                                                                                                                                                                                                                                                                                                                  Clone from S. Wiemann, Molecular Genome Analysis, German Cannessarch Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; Research Centre for Blotechnology sequenced by GBF (National Research Centre for Blotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                Key
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/mol_type="mRNA"
/roganism="Homo sapiens"
/clone="DKFZP779N169"
/clone=lib="779 (synonym: hnccl). V.
DH10B; sites SfiIA + SfiIB"
/dev_stage="fetal"
/tissue_type="liver"
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Tissue Procurement: Invitrogen
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587773"
/lab_host="DH10B"
                                                                                                                                                    inote="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: ECORV (destroyed); Site_2: Not1; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

352 t 4 others
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                                                             CAGCCTTCCTGCACCTTCCCGGCGGTTGGGTCCCTCCCCTCATGTAGTAAATCTCCCCCAC
                                                                                         roGlyValLeuGluLeuProArgValGlnVal----
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E..Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnMetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyr:::
||| :::||||||||:::|||:::||| ::::::
AGAAGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGT---ATAAAATGG
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TCCACAGTCTTGGGAAATGGCTCATCTCTGTGACTCCCAGAGGGCCAGTCTCTGCGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AspTrpThrGlySerThrProAlaTyrGlyTyrTrpPheLysAlaValThrGluThrThr 68
                      LeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeu
                                                                                                                                          {\tt AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrVall}
                                                                                                                                                                                                                                    ThrValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAsp 248
                                                                                                                                                                                                                                                                                       CATGGCACCAGCCTCACCTGTCAGGTGACCTTCCCTGGGGCCCAGCGTGACCAACAAG
                                                                                                                                                                                                                                                                                                                                  HisAspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArg
                                                                                                                                                                                                                                                                                                                                                                                    ---CTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCTCATCCCACAGCCCCAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCTGTGAGCAGGGGACACCCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCC---
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                                                                                                                                                                                            ACCGTCCATCTCAACGTGTCCTAC-
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/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
/note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;
Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Invitrogen). Research Genetics tracking
this is a NIH_MGC Library."
1 336 c 284 g 202 t 3 others
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                          Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Bataloy,S., Casavant,T., Kadota,K., Matsuda,H., Ashburner,M., Bataloy,S., Casavant,T., Kasukawa,T., Saito,R., Kas
                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muzamatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new of Genome Res. 10 (10), 1617-1630 (2000)
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2478 bp mRNA linear HTC 05-DEC-2002 Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-length enriched library, clone:E230037K16 product:SIALIC ACID-BINDING LECTIN SIGLEC-F homolog [Mus musculus], full insert
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Eutheria; Rodentia;
                  Gaasterland, T
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Kitsunai,T., Tashiro,H., Itoh,M.,
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translation="MGKENSHNCSLDIRDAQKIDTGTYFFRLDGSVKYSFQKSMLSVL"/
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanaqaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoka, T., Hirozane, T., Hari, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2478)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Please visit our web site for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                  /note="unnamed protein product; SIGLEC-F homolog [Mus musculus] FASTY, 95.9%ID, 100%length, matc
/protein_id="BAC39955.1"
/db_xref="GI:26352650"
                                                                                                                                                          putative"
                                                                                                                                                                                                                                                                                                                                                                                          429.
                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="oviduct"
/clone_lib="RIKEN full-length enriched mouse
/clov_stage="2 days pregnant adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="E230037K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FANTOM_DB:E230037K16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (6821), 685-690 (2001)
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lus] (SPTR|Q920G3, evidence:
    match=1770)
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Laboratory in R
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253 ProproGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGluAsnLeu 2	Qy 233 ArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsnThrProAsp 252	Qy 213 LeuThrCysH1sValAspPheSerArgLysGlyValSerAlaGlnArgThrValArgLeu 232	Qy 193 ThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHisAspThrAsp 212	Qy 173 CysProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGlyThrLysPro 192	Qy 153 ThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAlaPheGluGlu 172	Qy 133 AspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyrIleProGlu 152 :::	Qy 113 GluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMetAsn 132 	Qy 93 ThrGlyAspProAlaLysGlyAsnCysSerLeuVallleArgAspAlaGlnMetGlnAsp 112	Oy /3 VAIAIR'NTASH1SGINSETATGGINVAIGIUMETSETThTATGGIYATGPheGInLeu 92	53 SerThrProAlaTyveTepheLysAlaValThrGluThrThrLysGlyAlaPro	261	204 GGGTGCCTGCGCTGCGCTCCTCAGTGACTGGTTCAGTGACAGTGCAG	US-09-937-636-3 (1-512) x AK087658 (1-2478)	24.74% Indels: 11 Gaps:	Pred. No.: 1.21e-45 Length: 2478 Score: 669.50 Harches: 187 Percent Similarity: 43.37% Conservative: 78 Best Local Similarity: 30.61% Mismatches: 176	Scores:	OUNT 620 &	polyA_signal 2459. 2464 /note="putative" polyA_site 2478	YICOAONSQGAQTASVSLSIRSLVQLLGPSCSFEGQGLHCSCSSRAWPAPSLRWPLGE GVLEGNSSNGSFTVKSSSAGQWANSSLILSMEFSSUHRLSCEAWSDURVQRATILLYS GPKVSQAGKSETSRCTYLGAIWGAGLMALLAVCLCLIFFTVKVLRKKSALKVAATKGN HLAKNPASTINSASITSSNIALGYPMPGSSE"	VIALTEVPNIQVTSTLVSGNSTKLLCSVPWACEQGTPPIFSWMSSALTSLGHRTTLSS ELNLTPRPQDNGTNLTCQVNLPGTGVTVERTQQLSVIYAPQKMTIRVSWGDDTGTKVL QSGASLQIQEGESLSLVCMADSNPPAVLSWERPTQKPFQLSTPAELQLPRAELEDQGK
Qy 500 sGlyThrGlnAlaAspTyrAlaGluValLys 510 : :::::: :::	OY 480 UHISTYRALATNILGUASNPHEPIGGLYVALAIGPIGAIGPIGGLUALAAIGMEEPIGLY 500	1716 CCAGAAAGGACAGCCACCCTTGCCACAGTCCCAGACACCCAAAAGGATGAGCCTTAACT	10 Dystaliugabyaariitytariiteurio	150 TOCACCATACATACT TOCACCATACT TOCACATACT TOCACCATACT	1578CTGAAAGTAGCAGCTACGAAAGGCAACCATCTTGCCAAGAACCCTGCC	150 FLUTS ON THE STITLE STUTIL FLOOR SELECT STREET STATES OF THE STEEL STUTIL FLOOR SELECT STREET STATES OF THE STEEL STUTIL FLOOR SELECT STREET STATES OF THE STATES OF T	372 1503	1443 TCACAGGCAGCAAATCAGAAACCAGTAGAGGAACGGTCCTGGGGGGCCATCTGGGGAGCT	Db 1383 GCTTGGAGTGACAATAGAGTTCAGAGAGCCACTATCTTGCTGGTGTCAGGCCCAAAGGTC 1442	1323 GCCAACAGCTCCCT	Db 1263 CTGGAGGGGAACAGCAGCAATGGCTCCTTCACGGTTAAGTCCAGCTCCGCAGGACAGTGG 1322 Qy 358LeulleSerThralapheSerasn	Db 1203 AGCTGCTCCAGAGCCTGGCCTGCCCCTCCCTGCGCTGGGGGGAGGGGGTG 1262 Qy 357 357		Qy 352 352 Db 1143 AGGAGGCTTTGTACAGGTGTGTGTGTGTGTTGTTGTGAGGGTTAAGGTTTTGTACTTGT 1202	Qy 333 PheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerVal 352 :::		Ov 313 GlnProSerAspProGlvValLeuGluLeuProArgValGlnValGluHisGluGlvGlu 332	293 HisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSer	Qy 273 GlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThr 292 ::: :::	Db 852CCACAGAAGATGACCATCAGGGTGTCCTGGGGGAGATGACACAGGAACTAAAGTCCTG 908

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Query Match:
                                                                                                                                                                                                                                                                                                                       Score:
                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                            COUNT
                                                                                                                                                                                                                                                                                                                                    No.:
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                                            226
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              61
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                                                                                                                                   21
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12364 row: o column: 15
High quality sequence start: 64
High quality sequence stop: 538.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Invitrogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1745)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       вм906520.1 GI:19356899
      PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg
                                       TGCAACCTCTCCTACCCCGGGATGGCTGGGACGAGTCTACTGCTGCTTATGGCTACTGG
                                                     CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp
                                                                                                TACAGTCTTCAAGTGCAGAGGCAGGTGCCGGTGCCGGAGGGCCTGTGTGTCATCGTGTCT
                                                                                                                PheTrpIleArgValGluSerValMetValProGluGlyLeuCysIleSerValPro
                                                                                                                                                         CTGCTGCTGCTGCTGCTGCCGGTGCTGGGGGGGGGGGGTCCCTGAACAAGGATCCCAGT
                                                                                                                                                                             GGCTATGAAATCTGTATACACAGAGATCAAG 1863
                                                                                                                                                                                                                                                                                                                                                                                            362
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                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: Ovary (pool of 3); Vector: pCMV-SPORT6; Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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plate: LLAM12795 row: k column: 02
High quality sequence stop: 637.
Location/Qualifiers
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Tissue Procurement: Life Technologies,
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/tissue_type="leukocyte"
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                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12798 row: d column: 15
                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                                                                                                    5', mRNA sequence.
BM922958
                                                                                                                                                                                                                                                                                                                                                                                                                  BM922958 1012 NACENCOURT_6632090 NIH_MGC_118
                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                         BM922958.1
                                                                                                           CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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    AlaArgHisProLeuGly 342

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/organism="Homo sapiens'
                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 ATGCTGCCCTGCTGCTGCCCCCTGCTGCGGGGGGGTCCCCTGCAGGAGAAGCCAGTG
rArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAs
                                                                                                                                                                                                                                                                 ThrGlyAla-AlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGAGGAAGGGATGTAAAATATAGCTACCAACAGAATAAGCTGAACTTGGAGGTGACA
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                                                                       CACCCTCACCCCAGGCCCGAGGACCATGGCACCAACCTCACCTGTCAGGTGGAACGCCA
                                                                                                                                                                                                        ACGGGGGAATGCCCTCAGCCCC-----CTGGACCCCGAGACCACCCGCTCCTCGGAGCT
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/note="Vector: pCMV-SpORT6; Site_1: NotI; Site_2: EcoRV
/note="Vector: pCMV-SpORT6; Site_1: NotI; Site_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."
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/tissue_type="leukocyte"
/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 997)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
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                                                                                                                                      /note=Torgan: pooled brain, lung, testis; vector: pcMv-SpORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of male brains, age range 23-27; I male lung, age 27; and I male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Trivitronen Pascarch Canadiana traction and
                                                                                Gruber (Invitrogen). Research Genetics tracking 021. Note: this is a NIH_MGC Library."

314 c 266 g 201 t 1 others
                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5753477"
                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                 /lab_host="DH10B"
  6.17e-42
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Homo sapiens cDNA clone IMAGE:5753477
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   oSerAspPro 317
                                TCCCCCTGCCAGGCTGAGCTGGGAACCCGGAGGAATCTGACCCTTGTACCCCTCACAGGCC
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                                                                                                                                                                      AsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGly
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                                                           rProProAlaArgLeuSerTrp--ThrGlnArgGlyGlnValLeuSerProSerGln-Pr
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 864)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
http://image.llnl.gov
plate: NDAM363 row: g column: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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AspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMet 131
                                                                                                         CCAGTGGCCACAAACGACCCAGACGAAGAAGTGCAGGAGGAGACCCGGGGCCGATTCCAC
                                                                                                                           ProValAlaThrAsnHisGlnSerArgGluValGluMetSerThrArgGlyArgPheGln
                                              CTCCTCTGGGATCCCAGAAGGAAGAACTGCTCCCTGAGCATCAGAGATGCCCGGAGGAGG
                                                                LeuThrGlyAspProAlaLysGlyAsnCysSerLeuValIleArgAspAlaGlnMetGln
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/db_xref="taxon:9606"
/clone="IMAGE:30337798"
/tissue_type="pre-eclamptic p
/lab_host="DB10B_TonA"
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Search completed: October 8, 2003, 22:41:04 Job time : 3195 secs

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Title:
Perfect score:
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-MODEL-frame+_D2n.model -Dev=xlh
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-O-/cgn2_1/USPTO_spool/US09937636/runat_08102003_083237_29990/app_query.fasta_1.711
-DB-Issued_patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -STRATT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0937635_eCGM.10_1_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -NGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-468-8568-3

US-08-468-8568-2

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tent No. 5	e 123, Ap	equence 3, Appl	equence 118, Ap	equence 118, Ap	e 14	equence 14	e 14	e 14	14	Sequence 145, App	14	14	e 16	16	e 35	equence 2,	equence 16	equence 1,	equence 4,	equence 59	5	equence 66	equence 1, Appl	equence 1120, A	502, Ap	nce 2, Appl	tent No.	equence 72, App	e 31, App	equence 6, Appl	equence 30,	Sequence 6, Appli

ALIGNMENTS

; Sequence 3, Application US/09038832 ; Patent No. 6146845 ; GENERAL INFORMATION: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041
APPLICATION NUMBER: 197
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,03
REFERENCE/DOCKET NUMBER: 6 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA: APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Sialoadhesin TITLE OF INVENTION: (SAF-2) CITY: VA STATE: F COUNTRY: APPLICATION NUMBER: FILING DATE: 11-MAI ADDRESSEE: F: P.O. BOX 980 VALLEY FORGE 19482 PA USA RATNER & PRESTIA 11-MAR-1998 US/09/038,832 23,031 GH-50018 Family Member-2

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Query Match:
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INFORMATION FOR SEQ ID NO:
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LENOTH: 1597 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                               ValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsn
                                                                                                  GGCACCAGCCTCACCTGTCAGGTGACCTTGCCTGGGACAGGTGTGACCACGACCAGTACC
                                                                                                                               AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr
                                                                                                                                                                                   ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis
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                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                        ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNI
TITLE OF INVENTION: Sialoadhesin
TITLE OF INVENTION: (SAF-2)
                                                                                                                                                                STREET: VA
CITY: VA
STATE: F
COUNTRY:
APPLICATION NUMBER: FILING DATE: 11-MAI CLASSIFICATION:
                                                                                                 COMPUTER:
                                                                                                                                                                                                                                 ADDRESSEE: RATNER & PRESTIA
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Best Local Similarity:
Query Match:
DB:
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FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEPAX: 610-407-0701
TELEPAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2900 base pairs
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                    PheMetAsnAspGlyPhePheLeuLysValThrAlaLeuThrGlnLysProAspValTyr 149
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                       ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis
                                                                                           TGTAAGCAGGGGACACCCCCCATGATCTCCTGGATTGGGGCCTCCGTGTCCTCCCCGGGC
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Sequence 1, Application US/09046736

Patent No. 6090582

GENERAL INFORMATION:
APPLICANT: KIKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
APPLICANT: ERICKSON-MILLER, CONNIE
APPLICANT: SIGUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
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Best Local Similarity:
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SOFTWARE: FASTSED for Windows Version
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 1501 base pairs
TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION IMPORMATION:
TELEPHONE: 610-407-0700
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/0.
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
US-09-937-636-3 (1-512) x US-09-620-312D-407 (1-1488)
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LENGTH: 1488
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                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
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TITLE OF INVENTION: No. 6599662el Nucleic
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version
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Wang, Jian-Rui
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RESULT 6
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/760,031
FILING DATE: 13-SEP-1991
PRIOR APPLICATION NUMBER: US 07/274,107
APPLICATION NUMBER: US 07/274,107
FILING DATE: 21-NOV-1988
                                                                                                                     APPLICATION NUMBER: US 07/060,031
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/016,683
FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/896,361
APPLICATION NUMBER: US 06/896,361
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MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: ACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WORDER FECT 3.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CDNAS CODING FOR MEMBERS TITLE OF INVENTION: CARCINOEMBRYONIC ANTIGEN
                  REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.10-KGB
TELECOMMUNICATION INFORMATION:
                                                                 FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: KUTL G. Briscoe
                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/207,678 FILING DATE: 16-JUN-1988 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1339 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
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AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr---::::||| ||||||||||||||||||
                                                      ---AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT
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                                                                                                                                                                                                               RESULT 7
                                                                                                                                               Sequence 3, Application US/08468859A Patent No. 6022958 GENERAL INFORMATION:
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Horn Kramer &
STREET: 660 White Plains Road
                                                                        TITLE OF INVENTION: CDNAS CODING FOR TITLE OF INVENTION: CARCINOEMBRYONIC NUMBER OF SEQUENCES: 14
                                                                                                                 APPLICANT: Barnett, Thomas; APPLICANT: Kretschmer, Axel
   CITY:
STATE:
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New York
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                                                                                                                                 Barnett, Thomas; Elting, James; Kamarck, Michael;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07
FILING DATE: 19-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 19-FEB-1987
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WordPerfect 3.5

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 242.9-KGB
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 21-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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19-FEB-1987
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13-AUG-1986
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PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/207,678 FILING DATE: 16-JUN-1988 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/060,031 FILING DATE: 19-JUN-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/016,683 FILING DATE: 19-FEB-1987 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 06/896,361 FILING DATE: 13-AUG-1986 ATTORNEY/AGENT INFORMATION: NAME: Kurt G. Briscoe REGISTRATION NUMBER: 33,141	SOFTWARE: WordPerfect 3.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,856B FILING DATE: 06-JUN-1995 CLASSIFICATION: 424 FILING DATE: 06-JUN-1995 CLASSIFICATION DATA: APPLICATION NUMBER: US 08/027,974 FILING DATE: 08-MAR-1993 PRIOR APPLICATION DATA: APPLICATION UNMBER: US 07/760,031 FILING DATE: 13-SEP-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/274,107 FILING DATE: 21-NOV-1988	PALCER OF THE PALCE OF THE PALC	Db 1177

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                          ValArgLeuArgValAlaTyrAlaProArgAspLeu---ValIleSerIleSerArgAsp
                                                                                        GACACAACCTACCTGTGGTGGATAAACAATCAGAGCCTCCCGGTCAGTCCC------
                                                                                                                                AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr
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-AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT
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                                                                                                                                                                                                          ACCAACTTCAGCCTCCCCATCCCTAACAGCCACAGAAATAATTTATTCAGAAGTAAAAAA
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25 ValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	Qy 5 LeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheTrpIleArg 24 ::: Db 127 CTGCTCACAGCCTCACTTCTA	-937-636-3 (1-512) x US-08-468-859A-2 (1-1630)	6.91% Indels:	1. NO.: 2.208-00 re: 187.00 cent Similarity: 36.25%	ent Scores:	; TOPOLOGY: 11near US-08-468-859A-2	; SEQUENCE CHARACTERISTICS: ; LENGTH: 1630 nucleotides ; TYPE: nucleic acid ; STRANDEDNESS: single	FELEPHONE: (914) 332-1804 TELEPAX: (914) 332-1844 FINFORMATION FOR SEQ ID NO: 2:	NAME: Kurt G. Briscoe REGISTRATION NUMBER: 33,141 REFERENCE/DOCKET NUMBER: MDI 242.9-KGB	G DATE: 13-AUG-1986 Y/AGENT INFORMATION:	; FILING DATE: 19-FEB-1987 ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 06/896,361	19-JUN-1987 ION DATA: NUMBER: US 07/016,	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/060,031	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: US 07/207,678 ; FILING DATE: 16-JUN-1988	APPLICATION NUMBER: US 07/274,107 FILING DATE: 21-NOV-1988	:P-1991 'A:	PRIOR APPLICATION DATA: 03 00/02/,3/4 PRIOR APPLICATION DATA: APPLICATION MIMBER: IS 07/750 031	5 A:	APPLICATION NUMBER: US/08/468,859A FILING DATE: 06-JUN-1995	; OPERATING SYSTEM: SYSTEM 7.5 ; SOFTWARE: WORDPEFECE 3.5 ; CURRENT APPLICATION DATA:	TYPE: Diske	; COUNTRY: USA ; ZIP: 10591-5144 ; COMPUTER READABLE FORM:	STATE: New York	CORRESPONDENCE ADDRESS: 14 CARDESCEE: CONTROL OF STREET CONTROL ADDRESSEE: CONTROL OF STREET CONTROL O	TITLE OF INVENTION: CONSCIONEMBRYONIC ANTIGEN FAMILY	; GENERAL INFORMATION: ; APPLICANT: Barnett, Thomas; Elting, James; Kamarck, Michael; . APPLICANT: Kretschmer Avel
Qy	Db QQ	p Db	Qy	ab Cy) Db	Qy	Db Oy	DЬ	מם	Qy	D _D	Db	O _V	D Qy	Db	Qy	Db CY	ם ס	Qy	Db	Øy !	Dy Oy	Db Vy	⊋ Db	, Q	Db
358 LeulleSerThrAlaPheSer 364 :::	339 HISPTONEUGIYSEFGINHISVALSETLEUSETLEUSETVAIHISTYTLYSLYSGIY 337 ::: ::	CTCTTTATCCCTAACATCACTGTGAATAATAGTGGATCCTATACCTGCCACGCCAAT	319 ValLeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArg 338	299 ArgLeuserTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318 ::: 874 CAGTACTCCTGGCTTATCAATGGAACATTCCAGCAAAGCACACAAGAG921	TATTACCGTCCAGGGGCAAACCTCAGCCTCTCCTGCTATGCAGCCTCTAACCCCACCTGCA	283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla 298	268ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	249 ASDTERPYOASPPYOPYOGINASDLENAYGYBIMEVBAISEFGIDALBASDAYGTER 26/ :::	::::: :::	30 ValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAsp	210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229	:::	ThrIvsProThrThrSerHisPheSerValLeuSerPheThrProArdProGlnAspHis	170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189	495 495	150 IleProGluThrLeuGluProGlyGlnProValThrVallleCysValPheAsnTrpAla 169	130 rnemecksnaspelyrnerneleubysvalthralabeutnitsinbysrioaspealtyr 149 ::: ::: :::	CAGAATGACACAGGATTCTACACCCTACAAGTC	110 MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129		AlaLysGlyAsnCysSerLeuValIleArgAspAlaGln	77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96	262 GGCTACAGCTGGTACAAAGGGGAAAGAGTGGATGGC297	GTTCTTCTCCTTGTCCACAATCTGCCCCCAGCAA	CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr ::: :::	

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RESULT 10
US-08-468-856B-1
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          APPLICATION NUMBER: US/08/468,856B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/027,974
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
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tent No. 6013772
                                                                                                                                                                                                                                                             STREET: 000
CITY: Tarrytown
CTTATE: New York
TISA
                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
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                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inc
COMPUTER: APPLE MACINTOSH 6500
OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WORDERfect 3.5
 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                E: Sprung Horn Kramer & Woods
660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                              Barnett, Thomas; Elting, James; Kamarck, Michael; Kretschmer, Axel
VENTION: CDNAS CODING FOR MEMBERS OF THE VENTION: CARCINOEMBRYONIC ANTIGEN FAMILY
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US 07/760,031
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Best Local Similarity:
Query Match:
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INFORMATION FOR SEQ ID NO:
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REFERENCE/DOCKET NUMBER: MD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
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LENGTH: 3173 nucleotides
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APPLICATION NUMBER:
FILING DATE: 21-NOV-
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                                                                                                         MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129
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19-JUN-1987
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488 ProGlyValArgPro---ArgProGluAlaArgMetProLys-----GlyThrGlnAla 504
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                                                                              ThrGlnAlaProGluSerGlnGluSerGlnGluCeuHisTyrAlaThrLeuAsnPhe 487
                                                                                                                                                  SerLysLysAsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSer 467
                                                                                                                                                                                                                                           GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu 447
                                                                                                                                                                                                                                                                                        CAG-----GACCACTCCAAT-----
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                                                                                                                           AACAAGATGAAT - - - - -
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                                        Alignment Scores: Pred. No.:
                                                                                                     US-08-468-859A-1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Applic Patent No. 6022958
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: SYSTEM 7.5
SOFTWARE: WordPerfect 3.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/016,683 FILING DATE: 19-FEB-1987 PRIOR APPLICATION DATA:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3173 nucleotides
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Barnett, Thomas; APPLICANT: Kretschmer, Axel
                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                           TOPOLOGY:
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660 White Plains Road
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                                                                                                                           linear
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13-AUG-1986
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Length:
Matches:
Conservative:
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300 LeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyVal 319 	283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArg 299	268 ValleuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	249 AsnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267 :::	230 ValArgLeuArgValAlaTyrAlaProArgAspLeuValIleSerIleSerArgAsp 248 ::::::: ::: ::: ::: ::::	210 ASPThrASpLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229 589 GACACAACCTACCTGTGGTGGATAAACAATCAGAGGCCTCCCGGTCAGTCCC639	190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209 :::	170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189	150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla 169	130 PheMetAsnAspGlyPhePheLeuLySValThrAlaLeuThrGlnLysProAspValTyr 149 ::: :::	110 MetGlnAspGluSerGlnTyrPhePheArgValGluArgGlySerTyrValArgTyrAsn 129	97 AlaLysGlyAsnCysSerLeuVallleArgAspAlaGln 109	77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96 :::: ::::::	58 GlyTyrTrpPheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsn 76 	41CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57 ::: ::: :::	25 ValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	5 LeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArgPheTrpIleArg 24	3 Gaps:) x US-08-468-859A-1 (1-3173)	Best Local Similarity: 21.90% Mismatches: 180 Query Match: 6.84% Indels: 176
P	CURRENT APPLICATION NUMBER: US/08/468,856B PETTING NUMBER: US/08/468,856B	COMPUTER: APPLE MODERATION COMPUTER: APPLE M	CITY: CITY: STATE: COUNTI	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: Sprung STREET. 660 white	APPLICANT: Barnett, Thomas; Elting, James; Ke APPLICANT: Kretschmer, Axel APPLICANT: Kretschmer, Axel TITLE OF INVENTION: CDNAS CODING FOR MEMBERS TITLE OF INVENTION: CDNAS CODING FOR MEMBERS	Sequence Patent No	Qy 505 AspTyrAlaGluValLysPheGln 512 Db 1339 ATTTATTCAGAAGTAAAAAAGCAG 1362	Qy 488 ProglyValArgProArgProGluAlaArgMetProLysGlyThrGlnAla 504 ::: ::: ::: Db 1279 GAAGCCCAGCACACCACAACCAACTTCAGCCTCCCCATCCCTAACAGCCACAGAAATA 1338	Oy 468 ThrGinAlaProGluSerGinGluSerGinGluGluLeuHisTyrAlaThrLeuAsnPhe 487	1240	P	408 ThrIleLeuAspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsn	Qy 390ProLysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSer 407 :::	3/6 Leun : 1102 CTGG	359IleGerThrAlaPheSerAsnGlyAlaPheLeuGlyIleGlyIleThrAla	982 TCAGTCACTGGCTGCAACAGGACCACAGTCAAGACGATCATAGTCACTGATAATGCTCTA	922 CTCTTTATCCCTAACATCACTGTGAATAATAGTGGATCCTATACCTGGCACGCCAATAAC	Qy 320 LeuGluLeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHis 339

110 PheMetasnaspGlyPhePheLeuLysValThralaLeuThrGlnLysProaspValTyr	Db 352 GCAAACAGCGGTCGAGAGACAATATACCCCAATGCATCCCTGATCCAGAACGTCACC 411 Qy 110 MetGlnAspGluSerGlnTyrPhePheArqValGluArqGlySerTyrValArqTyrAsn 129		Oy 77 HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro 96 ::: ::::::	Qy 58 GlyTyrTrpPheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsn 76	Oy 41CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyr 57	Qy 25 ValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40 ::: :::	5 LeuLeuLeus	6.84% Indels: 3 Gaps: 3 Yus-08-468-8568-6 (1-3461)	Pred. No.: 1.2e-07 Length: Score: 185.00 Matches: 130 Percent Similarity: 34.65% Conservative: 80 Best Local Similarity: 21.45% Mismatches: 200	line	SEQUENCE CHARACTERISTICS: LENGTH: 3461 nucleotide TYPE: nucleic acid STRANDEDNESS: single	TELECOMMUNICATION INFORMATION: TELEPHONE: (914) 332-1700 TELEFAX: (913) 332-1844 TMFORMATION FOR SEO ID NO. 6.	2 - 5 -	FILING DATE: 19-FEB-198 PRIOR APPLICATION DATA: APPLICATION NUMBER: 13-AUG-198		PRIOR APPLICATION NU APPLICATION NU FILING DATE: PRIOR APPLICATIO			; FILING DATE: 08-MAR-1993 ; PRIOR APPLICATION DATA:
Db 1300 ATCATGCTGAACGTAAACTATAATGCTCTACCACAAGAAAATGGCCTCTCACCT 1353 Qy 442 GlyAla	422	Qy 418ThraladlyPro 421 Db 1240 GATGCTGGGACGTATTGGTGTGAGGGTCTTCAACCCAATCAGTAAGAACCAAAGCGACCCC 1299	1183 AGGATGAAGCTGTCCCAGGGCAACACCACCCTCAGCATAAACCCTGTCAAGAGGGAG		365ASNGIY	358 LeulleSeTThrAlaPheSer	339 HisproLeuGlySerGlnHisValSerLeuSerLeuSerValHisTyrLysLysGly ::: :: 979 AACTCAGTCACTGGCTGCAACAGGACCACAGTC	Qy 319 ValLeuGluLeuProArgValGlnValGluH1sGluGlyGluPheThrCysH1sAlaArg 338	Qy 299 ArgLeuSerTrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGly 318	Qy 283GlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAla 298	Qy 268ValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeuGlu 282	Qy 249 ASnThrProAspProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThr 267 ::: ::::::	Qy 230 ValargLeuargValalaTyrAlaProArgAspLeuValIleSerIleSerArgAsp 248 :::::: ::: :::: :::	Qy 210 AspThrAspLeuThrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThr 229	Qy 190 ThrLysProThrThrSerHisPheSerValLeuSerPheThrProArgProGlnAspHis 209 ::: ::: :::	Qy 170 PheGluGluCysProProProSerPheSerTrpThrGlyAlaAlaLeuSerSerGlnGly 189 Db 496CCGGAGCTGCCCAAGCCCTCCATCTCCCAGCAACCAAC 531	Db 495 495	150 IleProGluThrLeuGluProGlyGlnProValThrValIleCysValPheAsnTrpAla	Db 457 CTTCTGAAGGAAGAAGGAACTGGAACAGTTCCATGTATAC 495

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RESULT 13
US-08-468-859A-6
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                                                 FILING DATE: 19-FEB-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06,
FILING DATE: 13-AUG-1986
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
                                                                                                                                         PRIOR APPLICATION DATA:
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STREET: vv.
CITY: Tarrytown
CTATE: New York
TTATE: New York
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APPLICATION NUMBER:
FILING DATE: 19-JUN-
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APPLICATION NUMBER:
FILING DATE: 08-MAR-
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                                                                                                                                                                                                     APPLICATION NUMBER: US 07 FILING DATE: 16-JUN-1988
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 21-NOV-1988
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/760,031 FILING DATE: 13-SEP-1991
                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/468,859A FILING DATE: 06-JUN-1995
         REFERENCE/DOCKET NUMBER:
                         REGISTRATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
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                                       Kurt G.
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DB:
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TELEPHONE: (914) 332-1700
TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                  ---AGGCTGCAGCTGTCCAATGGCAACAGGACCCTCACTCTACTCAGTGTCACAAGGAAT
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                                                                                                                                                                                             TCCAATGACCCACCTAACAAGATGAATGAAGTTACTTATTCTACCCTGAACTTTGAAGCC
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; LOCATION:
US-08-408-095-30
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; Sequence 30, Application US/08408095
; Patent No. 5858678
                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-937-636-3 (1-512) x US-08-408-095-30 (1-2166)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202)293-7
TELEFAX: (202)293-786
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 2166 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mack, Susan J. REGISTRATION NUMBER: 30,951 TELECOMUNICATION INFORMATION: TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK &
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chinnadurai, Govindaswamy TITLE OF INVENTION: APOPTOPSIS-REGULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 21-MAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SUGHR
STREET: 2100 Pen
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C
            116 rPhePheArgValGluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePh 136
                                                   450 TGTCGCCCTGAATGTCCAGTATGCCCCCCGAGACGTGAGGGTCCGG-------
                                                                                                                                                                                                             346 TGGGA-GGAGCCATCGCTTGGGGTGCTGAAGATCCAAAACGTTGGCTGGGACAACACAAC
                                                                                                                                                                                                                                                                                                                                                                       238 ATTCAAAACCCCCATGCCGATTCGAGAAGGAGACACAGTGACCCTTTCCTGTAACTACAAT 297
                                                                                                                                                                                                                                                                                          298 TCCAGTAACCCCAGTGTTACCCGGTATGAATGG------AAACCCCCATGGCGCC
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                                                                                         AlaLysGlyAsnCysSerLeu-ValIleArgAspAlaGlnMetGlnAspGluSerGlnTy
                                                                                                                                  CATCGCCTGCGC----
                                                                                                                                                                    HisGlnSerArgGluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspPro
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Matches:
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	· 1313 AGAGACCTCCCCGGACCTGCGATGACACGGTCACTTATTCAGCATTGCACAAGCGCCAAG 1372	Db
20 000 Personal Control Contro	450LysAsnGlnL 453	Qy
) L	1253 CCCTGCGCTTTCCCGAGATGAACATACCACGAACTGGAGATGCAGAGTCCTCAGAGATGC 1312	Db
	431 hrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLys 449	Qy
	1193 AAGGCCCCCACTCCCTGGGATGCTACAATCCAATGATGGAAGATGGCATTAGCTACACCA 1252	Db
1/6	411 spTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAlaT 431	Qy
408	1133 ATTCCAGCGGCCAGAGCTTCTTTGTGAGGAATAAAAAGGTTAGAAGGGCCCCCCTCTCTG 1192	Db
157	399ProArgProArgPheSerArgHisSerThrIleLeuA 411	Qy
348	1073 GTGGGCTCAAGCTCCAGCGACGTTGGAAGAGGACACAGAGCCAGCAGGGGCTTCAGGAGA 1132	DЬ
138	389LeuProLysArgArgThrGlnThrGluThr 398	Qy
	1025 TGGCTGTGGGACTCGGGTCCTGCCTCGCCATCCTCATCCTGGCAATCT 1072	Dъ
Qy 120 ValGlu	euGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIle-	Qγ
Db 243 AATGGTTCCCTCC		ם ב
Qy 100 AsnCysSerLeuv	LeuSerValHisTvrLvsLvsGlvLeuIleSerThrAlaPheSerAsnGlvAlaPheL	Qy
US-09-937-636-3 (1-512) x t	330 IUG-VGIUFRETTRICYSHISAIAAATHISPTOLEUGI-YSETGINHISVAISETLEUSET- 349	윰 성
		}
Percent Similarity: 33. Best Local Similarity: 23.	errroserGinProserAspProGiyValLeuGiuLeuProArgValGLnValGiuHisG	g 5
	CCAACCCTCCCGTCTCCCACTACACCTGGTTTGACTGGAATAACCAA	ם מ
Alignment Scores:	294 erSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuS 310	Qy
; ORGANISM: Murine US-09-638-649-6		Db
ENGTH: 1348	274 snGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCysValThrHisS 294	Qy
SEO ID NO 6	774 774	DЬ
CONSENT REFLECTION NO.	254 roGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGluAsnLeuGlyA 274	Qy
FILE REFERENCE: 0575/63; FILE REFERENCE: 0575/63; CHESSENT ASSITCATION NUMBER	728 TGCTGTATGCACCCAGGAGGCTGCGTGTGTCCATGAGCCCGGGGGAC 774	Db
FITTLE OF INVENTION: GLY	234 alAlaTyrAlaProArgAspLeuValIleSerIleSerArgAspAsnThrProAspProP 254	Qy
		DЪ
; GENERAL INFORMATION: ; APPLICANT: Stern, David	214 hrCysHisValAspPheSerArgLysGlyValSerAlaGlnArgThrValArgLeuArgV 234	Qy
; Sequence 6, Application 0; Patent No. 6563015	622	ДЪ
RESULT 15 US-09-638-649-6	194 rSerHisPheSerValLeuSerPhe-ThrProArgProGlnAspHisAspThrAspLeuT 214	Qy
Db 1454 GGGAGCGGCCTCA	579 CCAGTTCTTCTGGGAGAAAAATGGCAGGCTTCTGGGGAAAGAA 621	Db
491	176 oSerpheSerTrpThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrTh 194	Qy
1411		Db
Qy 471 roGluSerGlnGl	oGlyGlnProValThrValIleCysValPheAsnTrpAlaPheGluGluCysProProPr	Оу
Db 1373 TGGGCGACTATG		dd '
Qy 453 ysLysGlnTyrG	eLeuLvsValThrAlaLeuThrGlnIvsProAspValTvrTleProGluThrLeuGluDr	0ν
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	ted: October 8, 2003, 22:42:57 9 secs	Search completed: Oc Job time : 139 secs	Sea
	CAGTCAGAGGAAGCGGAGATGCCAGAG 1196	1170	В
	ProGlyValArgProArgProGluAlaArgMetProLys 500	488	δ
1169	CTTGCAGAGCCAGGAGGAGGAGGAGGAGGAGGGAGGAGAGGGGAGAGGGGAGA	1125	망
487	ThrGlnAlaProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPhe	468	ρ
1124	GAGAGGAAG	1116	В
467	SerLysLysAsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSer	448	δ
1115	CAA	1101	망
447	GlnLysAlaThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGlu	428	Ş
1100		1074	рь
427	euAlaGlnLysA	408	Ş
1073		1073	В
407	${\tt IleLeuProLysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSer}$	388	οy
1073	CTGGGAGGCTGGGAGTAGCCCTGCTC	1044	망
387	PheLeuGlyIleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLys	368	δ
1043	CCAGCTGAAGGCTCTGTGGGTGAGTCTGGGCTTGGGCTAGCCCTTGGCGTTC	984	밁
367	LysLysGlyLeuIleSerThrAlaPheSerAsnGlyAla	355	δō
983	CACGGACCTCAGGAAAGCCCTCCTGTCAGCATCAGGGTCACAGAAACCGGCGATGAGGGG	924	Вþ
354	GlySerGlnHisValSerLeuSerValHisTyr	342	δ
923	CTCCCTGAGGTGGGGCACGCGGATGAGGGGCACCTATAGCTGCGTGGCCACCCAC	864	DВ
341	LeuProArgValGlnValGluHisGluGlyGluPheThrCysHisAlaArgHisProLeu	322	Ş
863	TGGATAAAGGATGGTGCACCCTTGCCCCTGGCTCCCAGCCCTGTGCTGCTC	813	Вb
321	${\tt TrpThrGlnArgGlyGlnValLeuSerProSerGlnProSerAspProGlyValLeuGlu}$	302	οy
812	CCTGGTGGGACCTTGACCTGTGCCATCTCTGCCCAGCCCCCTCCTCAGGTCCAC	753	뫄
301	GluGlyGlnSerLeuCysLeuValCysValThrHisSerSerProProAlaArgLeuSer	282	Q
752	GAGCCTGAAGGTGGAATAGTCGCT	729	망
281	SerGlnAlaAsnArgThrValLeuGluAsnLeuGlyAsnGlyThrSerLeuProValLeu	262	Q
728		684	B
261	VallleSerIleSerArgAspAsnThrProAspProFroGluAsnLeuArgValMetVal	242	Qy
683	CTGGGCCTTCCCCGGCGCAGACCCCTGAACACA	636	밁
241	LysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyr	222	φ

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27, 148, 1, A 258, 258,

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-MODEL-frame+_p2n.model -DEV-x1h
-Q-/cgn2_1/USSTO_spool/US09937636/runat_08102003_083237_24/app_query.fasta_1.711
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cd1 -LIST=45 -DOCALION=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LCALL -OUTFMY=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US09937636_@CGN_1_1_271_@runat_08102003_083237_24
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARM_TIMEOUT=90 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                 Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   2580.5
                                 Score
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                Match Length DB
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2706
                                                 Query
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   95.4
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Listing first 45 summaries
                                                                                                                                                                         : /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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                              Description
 Sequence 15, Appl
                                                         APPLICANT: LONGDATE, MALINDA
APPLICANT: LONGDATE, MALINDA
APPLICANT: Chang, Han
APPLICANT: Whitney, Gena
TITLE OF INVENTION: NOVEL SIGLECS AND USES THEREOF
FILE REFERENCE: DO003NP
CURRENT APPLICATION NUMBER: US/09/910,600
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/220,139
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 2208
TYPE: DNA
ORGANISM: Homo saplens
US-09-910-600-15
                                                                                                                                                                                                                                                                                                                       US-09-910-600-15
; Sequence 15, Application US/09910600
; Publication No. US20030036631A1
; GENERAL INFORMATION:
                Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
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2265
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US-09-978-824-258

US-09-918-585A-258

US-09-978-193A-258

US-09-978-757A-258

US-09-978-757A-258

US-09-978-643A-258

US-09-978-375A-258

US-09-978-375A-258

US-09-978-375A-258

US-09-978-375A-258

US-09-978-188A-258

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Qy 496 AlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLysPheGln 512	B AGCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAG	2038 TATCAGTITCOCAGAACCCAATCATCACTCAAGCCCCAGAATCCCAGGAG 2038 TATCAGTTGCCCAGTTTCCCAGAACCCCAATCATCACTCAAGCCCCAGAATCCCCAGGAG 2038 TATCAGTTGCCCAGTTTCCCAGAACCCCAATCATCACTCAAGCCCCAGAATCCCCAGGAG	20	416 1918	6 ThrGluThrProArgProArgPheSerArgHisSerThrTleLeuAspTyrIleAsnVal 4	LeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuProLysArgArgThrGln	OY 356 LYSGLYLEUILESETTHTALAPHESETASHGLYALAPHELGUGLYLLEGLYLLETHTALA 3/5	1678 TGTGAGGCCTGGAACGTCCATGGGGCCCAGAGTGGATCCATCC	1618 CCCTGGGCCAACAGCTCCCTGAGCCTCCATGGAGGGCTCAGCTCCGGCCTCAGGCTC	Db 1558 GAGCTGCTGGAGGGGAACAGCAGCCAGGACTCCTTCGAGGTCACCCCCAGCTCAGCCGGG 1617 Qy 354 354	Db 1498 CACTGCAGCTGCTCCCCAGGCCAGCCCGGCCCCTCTCTGCGCTGGTGGCTTGGGGAG 1557 Qy 354 354		331 0 1378 0 351 0	11 ProSerGlnProSerAspProGlyValLeuGLULeuProArgValGlnValGluHLSGlu	#AITNTHISSETSETPTOPTOALAATGLEUSETTTPTNTGLTAATGGLYGLNVALLEUSET 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2/1 ASILEUGIAASINGIAYINI SETLEUFIVAALUUI VALIBERLEUUVALUVALUUI III III III III III III III III III	1078 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG 253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu

	B & B & B & B & B & B & B & B & B & B &	Qy 181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200 ·	OY 161 ThrVallieCysValPheAsnTrpAlaPheCluGluCysProProSerPheSerTrp 180	549 GCCCTGACTCAGAAGCCTGATGTCTACATCCCCGAGACCCCTGGAGCCCGGGCAGCCCGTG 6	0y 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	Oy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	429 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 4	101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 1	Db 369 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC 428	1 G1uV	Db 309 TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 368	249 TGCTCTTCCCTACCCCCGACAAGACTGGACAAGGTCTACCCCCAGCTTATGGCTACTGG 3	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	Db TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC 248	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	129 ATGCTACTGCCACTGCTGCTGCTGCTGGGGGGGTCCCAGGCTATGGATGG	0v	-00-037-636-3 /1-513) v HS-00-010-600-37 /1-203/	Query Match: 95.36% Indels: 185	t Similarity:	Length:	-	OTHER INFORMATION: Description of Artificial Sequence: L3-995-2		LENGTH:	SOFTWARE: PatentIn Ver. 2.0	PRIOR FILING DATE: 2000-0	CURRENT FILLING DATE: 2001-07-20 PRIOR APPLICATION NUMBER: 60/220,139	FILE REFERENCE: DOOSNP CHRENT APPLICATION NIMBER: HS/09/910 500	: APPLICANT: Whitney, Gena : TITLE OF INVENTION: NOVEL STGIEGS AND HEREPOF	APPLICATE LONGSTON Malinda	Sequence 27, Publication	US-09-910-600-27
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TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: pF489p2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR APPLICATION NUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (3)
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LOCATION: (6)
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          PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg
                                                       CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp
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291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer		1041 CAGCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 252 1101 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC	241 LeuVallleSerIleSerArgAspAsnThrProAsp		141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal	81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn
310 ; FILE REFERENCE: D0003NP CURRENT APPLICATION NUMBER: US/09/910,600 ; CURRENT FILING DATE: 2001-07-20 ; PRIOR APPLICATION NUMBER: 60/220,139 PRIOR FILING DATE: 2000-07-21 ; NUMBER OF SEQ ID NOS: 32 1460 ; SOFTWARE: Patentin Ver. 2.0 ; SOFTWARE: DATE: DNO 350 ; TYPE: DNA 1520 ; ORGANISM: Homo Sapiens US-09-910-600-1	1220 RESULT 4 270 US-09-910-600- Sequence 1, Publication 1280 Publication GENERAL INFO 290 APPLICANT: APPL	Db 2121 TATCAGTTGCCAGTCTCCAGAATCCATCCAGGAGTCCAGAATCCAGGAGGAG CTCGTCCCATCCC 1100 Qy 476 SerGInGluGluLeuHisTyrAlaThrLeuAsnPheProGlyValArgProArgProGlu	252 Db 2001 980 Oy 436 252 Db 2061 1040 Oy 456	Db 1821 C 800	160 Db 1701 680 Qy 355 180 Db 1761 740 Db 1761 740 Qy 356	OALALYSGIYASN 100

252	79	252	Qy 252	Qy 241 LeuVallleSerIleSerArgAspAsnThrProAsp	Qy 221 ArglysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp	Qy 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer		Qy 161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp	Qy 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal	Qy 121 GluargGlySerTyrValargTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 	Qy 101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal	Qy 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn	Qy 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg	Qy 41 CysserPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro	euLeuProLeuLeuLeuSerSerLeuLeu 	84.188 11 6-3 (1-512) x US-09-910-60	2278.00 Matches: 4 it Similarity: 75.25% Conservative: 1 cocal Similarity: 75.08% Mismatches: 1	oo Toogeth.
APPLICANT: Desnoyers, APPLICANT: Eaton, Dar APPLICANT: Ferrara, 1	APPLICANT: Botstein	; GENERAL INE	252 US	252 Db 1755 TTCCAA 1	Qy	220	Qy 451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla	18 54	Qy 411 AspTyrILeAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 430 1160	140 140	120 Qy 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro	100 Qy 351 SerYalHisTyrLyscLyscLyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 100	80 Oy SI GLYGLUFFIETT CYSHISALARIGH SFIOLEUG LYSEIGHIBL SVALARIGH SFIOLEUG LYSEIGHIBL SVALARIGH SFIOLEUG LYSEIGHIBL SVALARIGH SFIOLEUG LYGE SFIELD GENERAL SFIELD GENER	Oy 311 ProSerGinProSerAspProGlyValIcuelDroArgValGinValGiuHisGiu 60	40	Qy 271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys 20	Qy 253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG	Db 855 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 914

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ETILE REFERENCE: P2630PICII

CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 09/91858

PRIOR PPLICATION NUMBER: 09/91858

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/06220

PRIOR FILING DATE: 1997-11-3

PRIOR APPLICATION NUMBER: 60/06311

PRIOR APPLICATION NUMBER: 60/06311

PRIOR APPLICATION NUMBER: 60/06364

PRIOR FILING DATE: 1997-11-3

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/077632

PRIOR APPLICATION NUMBER: 60/077641

PRIOR APPLICATION NUMBER: 60/077791

PRIOR APPLICATION NUMBER: 60/077791
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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      OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-13
OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078930
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR APPLICATION NUMBER: 60/079294
OR FILING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
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OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079726
OR APPLICATION NUMBER: 60/07920
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Fong, Sherman
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OR APPLICATION NUMBER: 60/083336
OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/083392
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083495
OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/08359
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OR APPLICATION NUMBER: 60/08359
OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/08359
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OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082700
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082797
OR FILING DATE: 1998-04-22
OR APPLICATION NUMBER: 60/082796
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OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081838
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/082568
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR APPLICATION NUMBER: 60/082569
OR APPLICATION NUMBER: 60/082704
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OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081203
OR APPLICATION NUMBER: 60/081229
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081955
OR FILING DATE: 1998-04-15
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DR FILING DATE: 1998-03-31
DR APPLICATION NUMBER: 60/080327
DR FILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/080328
DR FILING DATE: 1998-04-01
DR APPLICATION NUMBER: 60/080333
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FILING DATE: 1998-03-31
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FILING DATE: 1998-03-31
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
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FILING DATE: 1998-03-31
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Db 286 GGGTGDAATGACCCCCGGGGCCCAATCCCCCCTCGGGCATCCCCCAAGGGAATCCACCCCAAGGGAATCCACCCCCAAGGGAATCCACCCCCAAGGGAATCCACCCCAAGGGAATCCACCCCAAGGGAATCCACCCCAAGGGAATCCACCCCAAGGGAATCCACCCAAGAGACCCCAAGAGACCACCCCCAAGGACCACC	Alignment Scores: Pred. No.: 2265.00 Antches: 450 Percent Similarity: 74.92% Best Local Similarity: 14.75% Best Local Similarity: 74.75% Indels: 148 229 148 29 148 29 20	RIOR AP RIOR A
	252 832 . 253 . 253 892 271 952 291 1012 311 1072 331 1132	286 101 346 121 406 1414 465 161 465 201 472 221 532 532 241 592 252 772

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RESULT 6
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PA530PLC27
CURRENT APPLICATION NUMBER: US/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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                                                                                                                                                                                                                                      Paoni,
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Hillan, Kenneth J
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OR FILING DATE: 1998-03-26
OR APPLICATION NUMBER: 60/079664
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079689
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OR APPLICATION NUMBER: 60/079683
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/079786
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079920
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OR FILING DATE: 1998-03-12
OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-13
OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078936
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/078910
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DR FILING DATE: 1998-04-08
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DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081195
DR FILING DATE: 1998-04-08
DR APPLICATION NUMBER: 60/081203
DR FILING DATE: 1998-04-09
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DR APPLICATION NUMBER: 60/080327

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DR APPLICATION NUMBER: 60/080333

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REFILING DATE: 1997-10-17
DR APPLICATION NUMBER: 60/064249
REFILING DATE: 1997-11-03
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
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FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080194
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FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-15

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APPLICATION NUMBER: 60/085582
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{\tt ArgLysGlyValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp}
                                  ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu
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                                                                                                                                    {\tt ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp}
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OR APPLICATION NUMBER: 60/083496
OR FILING DATE: 1998-04-29
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OR FILING DATE: 1998-04-29
OR APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29

DR FILING DATE: 1998-04-22

DR APPLICATION NUMBER: 60/082700

DR FILING DATE: 1998-04-22

DR APPLICATION NUMBER: 60/082797

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DR APPLICATION NUMBER: 60/082796

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APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-29

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DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30
DR APPLICATION NUMBER: 60/084366
DR FILING DATE: 1998-05-05
DR APPLICATION NUMBER: 60/084414
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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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Grimaldi, J. Christopher
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OR APPLICATION NUMBER: 60/081955
DR FILING DATE: 1998-04-15
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FILING DATE: 1998-04
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Botstein, David
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Gao, Wei-Qiang
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
                   Godowski, Paul J.
Grimaldi, J. Christopher
                                                                Filvaroff, Ellen
                                 Gerritsen, Mary
Goddard, Audrey
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Wood, William
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411 ASpTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla 4	GAGAGAG
391 LysargargThrGLnThrGLuThrProArgProArgPheSerArgHLsSerThrILeLeu 	121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 1
	Qy 101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120
	Qy 81 GluWetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100
351 GGTV31UFINETHILCYSNISALGALIGHISFICUEUGLYSELGLINIISYGISELGEUGELGEUGL 	Qy 61 PheLysalavalThrGluThrThrLysGlyalaProValAlaThrAsnHisGlnSerArg 80
1 2 1	TyrglyTyrTrp 60 TATGGCTACTGG 225
	o 40 1 C 165
271 AsnieuciyasnolythrSerieuProvalieuciuciycinSerieuCysleuValCys	Qy 1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20
253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu	ch: 83.70% Indels: 10 Gaps: -636-3 (1-512) x US-09-999-832A-258 (1-2764)
832 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTG	t Similarity: 74.92% Conservative: 1 Ocal Similarity: 74.75% Mismatches: 3
252	: 9.93e-221 Length: 2265.00 Matches:
772 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC	lignment Scores:
252	PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION NUMBER: 60/085
712 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC	PRIOR APPLICATION NUMBER: 60/0857
252	PRIOR APPLICATION NUMBER: 60/08557
652 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC	PRIOR FILING DATE: 1998-05-15 PRIOR APPLICATION WITHBER: 60/08558
252	PRIOR FILING DATE: 1998-05-15 PRIOR FILING DATE: 1998-05-15
241 LeuvalileSerIleSerArgaspasnThrProAsp	DATE: 1998-05-15 FION NUMBER: 60/08570 DATE: 1998-05-15 FION NUMBER: 60/08568
221 ArglysglyvalSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 	PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/08532 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/08558
201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 	PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/0853 PRIOR FILING DATE: 1998-05-13 PRIOR APPLICATION NUMBER: 60/0853
181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu	PRIOR FILING DATE: 199 PRIOR APPLICATION NUME PRIOR FILING DATE: 199 PRIOR APPLICATION NUME
465	PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/08460
$161\ {\tt ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp}$	PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/0845
465	PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/0846
$141\ \verb AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal $	FILING DATE: 19

CURRENT CURRENT CURRENT CURRENT PRIOR PRIO	RESULT 9 US-09-978-189-25; Sequence 25, Publication No. GENERAL INFORM APPLICANT: Asl APPLICANT: BA APPLICANT: BA APPLICANT: BA APPLICANT: FE APPLICANT: FE APPLICANT: GA	Db 1372 Qy 431 Db 1432 Qy 451 Db 1492 Qy 471 Db 1552 Qy 491 Db 1612 Qy 511
NT APPLICATION NUMBER: US/09/978,189 NT FILING DATE: 2001-10-15 APPLICATION NUMBER: 09/91895 FILING DATE: 2001-07-30 APPLICATION NUMBER: 60/062250 FILING DATE: 1997-10-17 APPLICATION NUMBER: 60/064249 FILING DATE: 1997-11-03 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13 APPLICATION NUMBER: 60/06364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/06364 FILING DATE: 1997-11-21 APPLICATION NUMBER: 60/077450 FILING DATE: 1998-03-10 APPLICATION NUMBER: 60/077632	SULT 9 -09-978-189-258 -09-978-189-258 Sequence 258, Application US/09978189 Publication No. US20030004102A1 GENERAL INFORMATION: APPLICANT: Bakker Kevin P. APPLICANT: Bakker Kevin P. APPLICANT: Bectein, David APPLICANT: Bectein, David APPLICANT: Bectein, David APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan APPLICANT: Gao, Wei-Oiang APPLICANT: Good, Sherman APPLICANT: Goodward, Audrey APPLICANT: Goodward, Audrey APPLICANT: Goodward, Audrey APPLICANT: Goodward, Audrey APPLICANT: Gurney, Austin L. APPLICANT: Gurney, Austin L. APPLICANT: Kuo, Sophia S. APPLICANT: Kijavin, Ivar J. APPLICANT: Kuo, Sophia S. APPLICANT: Rapier, Mary A. APPLICANT: Rapier, Mary A. APPLICANT: Bacin, Nicholas F. APPLICANT: Shelton, David L. APPLICANT: Shelton, David L. APPLICANT: Stewart, Timothy A. APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Acids Encoding the Same	
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GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCTCCTCTGTGCTGCTGACAGC
                                                                                               GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAAC
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; ORGANISM: Homo
US-09-978-608A-258
                                                                                                                                                                                                                                                     US-09-937-636-3 (1-512) x US-09-978-608A-258 (1-2764)
                                                                                                                                                                                                                                                                                    Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                  Score:
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                                                                                                                                                                                                                                                                                                                                                                                                             Prior
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TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/978,608A CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrappen
                                                                                                                                                                                                                                                                                                                                                                                         Q ID NO 258
LENGTH: 2764
   346
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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Grinaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kijavin, Ivar J.
Kuo, Sophia S.
 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120
                                        PheLysalaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg
                                                                                                                                      CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp
                                                                                                                                                                                PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                             TGCTCTTTCTCCTACCCCCGACAAGACTGGACAGGGTCTACCCCCAGCTTATGGCTACTGG
                                                                                                                                                                      TTCTGGATACGAGTGCAGGAGTCAGTGATGGTGCCGGAGGGCCTGTGCATCTCTGTGCCC
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Filvaroff, I
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Wood, William
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Gerritsen, Mary E
Goddard, Audrey
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Gao, Wei-Qiang
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Matches:
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331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu	271 ASDICUCLYSTACTORY THE SCRIEDURO PROVIDED TO THE PROVIDED THE PROVIDED TO THE PROVIDED TO THE PROVIDED TO THE PROVIDED THE PROVIDED TO THE	252 252 832 TACACCTGCGAGCGGAGAACAGGCTTGGCCCGGGGTGAAGGCTCTGGGGATTCAGGGCGC 831 253 TACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCCAG	GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGGCTCCTCTGTGCTGCTGACAGC CAGCCCCCTGCCACACTGAGCTGCGTCCTGCAGAACAGAGTCCTCCTCCTCCTCCATCCC	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220		121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C15 CURRENT APPLICATION NUMBER: US/09/978,585A CURRENT FILING DATE: 2001-10-16 NUMBER OF SEQ ID NOS: 624 Prior Application removed - See File Wrapper or Palm SEQ ID NO 258 LENGTH: 2764 TYPE: DNA ORGANISM: Homo Sapiens US-09-978-585A-258	T: Kljavin, Ivar J. T: Kuo, Sophia S. T: Napler, Mary A. T: Pan, James; T: Paoni, Nicholas F. T: Paoni, Nicholas F. T: Roy, Margaret Ann T: Shelton, David L. T: Stewart, Timothy A. T: Stewart, Timothy A. T: Williams, P. Mickey T: Williams, P. Mickey T: Wood, William I.	APPLICANT: Filvaroff, Ellen APPLICANT: Fong, Sherman APPLICANT: Gao, Wei-Qiang APPLICANT: Gerber, Hanspeter APPLICANT: Geritsen, Mary E. APPLICANT: Goddard, Audrey APPLICANT: Goddard, Audrey APPLICANT: Gormaldi, J. Christopher APPLICANT: Gurney, Austin L. APPLICANT: Hillan, Kenneth J	5A.	Db 1552 CCAGAATCCCAGGAGGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTC 1611 Qy 491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510	411 AspTyrIleAsnValValProThrAlaGlyProLeuAlaGlnLysArgAsnGlnLysAla	Qy 391 LysArgArgThrGlnThrGluThrProArgProArgPheSerArgHisSerThrIleLeu 410

772 TGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGGCTGGGGATTCAGGGCGC 83	252	712 CAGCCCCCTGCCACACTGACCTGCGTCCTGCAGAACAGAACAGAGTCCTCTCTCT	07 252 252	252	92	Qy 241 LeuValIleSerIleSerArgAspAsnThrProAsp 252	Qy 221 ArgLysG1yValSerAlaGlnArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240	Qy 201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220 :::	Db 466	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 2	Qy 161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProSerPheSerTrp 180 Db 465 465	Db 465 465	Qy 141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 160	Qy 121 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr 140	Db 346 TGCTCCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCACAGTACTTCTTTCGGGTG 405	Qy 101 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 120	Qy 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100	Db 226 TTCAAAGCAGTGACTGAGACCAAGGGTGCTCCTGTGGCCACAAACCACCAGAGTCGA 285	100 TOUTTHUTUUTACUCCUGACAAGACTIGACAAGGTTCTACCCCCAGCTTAIGGCTACTGG 2	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	Db 106 TTCTGGATACGAGGGAGGCAGGAGGGAGGGCCTGTGCATCTCTGTGCCC 165	31 Dbodrational and incompleted the process of the	QY 1 MetLeuLeuProLeuLeuSerSerLeuLeuGlyGlySerGlnAlaMetAspGlyArg 20	US-09-937-636-3 (1-512) x US-09-978-585A-258 (1-2764)	11 Gaps:	Similarity: 74.92% Conservative: 1 al Similarity: 74.75% Mismatches: 3	9.93e-221 Length: 2265.00 Matches:
	; APPLICANT: Desnoyers, Luc ; APPLICANT: Eaton, Dan		; FUDITICACION NO. USZOUJUJUJUJUJUJUJUJUJUJUJUJUJUJUJUJUJUJUJ	US-09-978-191A-258 ; Sequence 258, Application US/09978191A	RESULT 12	Qy 511 PheGLn 512 	491 AIGHION 1612 AGACCCA	1552 CCAGAATCCCAGGAGAGCCCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTC	Db 1492 AACCAGAAAAGCAGTATCAGTTGCCCAGTTTCCCCAGAACCCAAATCATCACCCAAGCC 1551 Oy 471 ProgluSerglnGluSerglnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVal 490	451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla	1432 ACACCAAACAGTCCTCGGACCCCTCCTCCACCAGGTGCTCCCCCAGAATCAAAGAAG	431 ThrProAsnSerProArqThrProLeuProProGlyAlaProSerProGluSerLysLys	QY 411 ASPTYVI1eASNVALVALFYOTIALAGGLYPYOLEUALAGINLYSAGASNGLINLYSALA 430	1312 AAGAGACGGACTCAGAAAACCCCGAGGCCCAGGTTCTCCCGGCACAGCACGATCCTG	AleggericateggericiietiiiteeleargProArgPhoSerArgHtsSorThrT]eLen	Qy 371 IleGlyIleThrAlaLeuLeuPheLeuCysLeuAlaLeuIleIleMetLysIleLeuPro 390		1132 GGAGAGTTCACCTGCCACGCTCGGCACCCACTGGGCTCCCAGCACGTCTCTCTC	Qy 331 GlyGluPheThrCysHisAlaArgHisProLeuGlySerGlnHisValSerLeuSerLeu 350	Qy 311 ProSerGlnProSerAspProGlyValLeuGluLeuProArgValGlnValGluHisGlu 330	1012 GTCACACACAGCAGCCCCCCAGGCTGAGCTGGACCCAGAGGGGACAGGTTCTGAGC	Qy 291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	952 AACCTTGGGAACGGCACGTCTCTCCCAGTACTGGAGGGCCAAAGCCTGTGCCTGGTCTGT	271 AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	Db 892 CAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTCCCCAAGCAAACAGGACAGTCCTGGGAA 951	832 TACACCTGCCGAGGAGAACAGGCTTGGCTCCCAGCAGCCATCCTGTGACCTCTCTGTG	Qy 252 252

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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 1997-10-17
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PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065364
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1997-11-21
PRIOR PILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
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OR FILING DATE: 1998-03-11
OR APPLICATION NUMBER: 60/077791
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OR APPLICATION NUMBER: 60/078004
OR FILING DATE: 1998-03-13
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OR APPLICATION NUMBER: 60/078936
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Williams, P. Mickey
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Shelton, David L.
Stewart, Timothy A.
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Grimaldi, J. Christopher
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Hillan, Kenneth J
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DR APPLICATION NUMBER: 60/083559
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DR APPLICATION NUMBER: 60/083500
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DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/083392

DR FILING DATE: 1998-04-29

DR APPLICATION NUMBER: 60/083495

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PR APPLICATION NUMBER: 60/082704

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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
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FILING DATE: 1998-04-08
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081070
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FILING DATE: 1998-04-01
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FILING DATE: 1998-03-31
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81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 	Qy 61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 80	QY 41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60	Qy 21 PheTrpileArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	ProLeuLeuLeuSerSerLeuLeuG CACTGCTGCTGCTCGCTGCTGCTG	83.70% Indels: 11 Gaps: 2) x US-09-978-191A-258 (1-2764)	nt Similarity: 74.92% Conservative: 1 Local Similarity: 74.75% Mismatches: 3	Length:	; PRIOR FILING DATE: 1998-05-15; PRIOR APPLICATION NUMBER: 60/085697		FILING DATE: 1998-0 APPLICATION NUMBER:	FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08558	FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08557	FILING DATE: 1998-05-15 APPLICATION NUMBER: 60, FILING DATE: 1998-05-15 APPLICATION NUMBER: 60,	; PRIOR FILING DATE: 1998-05-13 ; PRIOR APPLICATION NUMBER: 60/085323 ; PRIOR FILING DATE: 1998-05-13 ; PRIOR APPLICATION NUMBER: 60/085582		; PRIOR FILLING DATE: 1998-05-07 ; PRIOR APPLICATION NUMBER: 60/084627 ; PRIOR FILLING DATE: 1998-05-07 ; PRIOR APPLICATION NUMBER: 60/084643	FILING DATE: 1998-05-0 APPLICATION NUMBER: 60	FILING DATE: 1998-05-07 APPLICATION NUMBER: 60,	NUMBER: 6 1998-05-	APPLICATION FILING DATE	FILING DATE: 1998-05-06 APPLICATION NUMBER: 60, ETITING DATE: 1998-05-06	ER: 60 8-05-0	
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351 SerValHisTyrLysLysGlyLeuIleSerThrAlaPheSerAsnGlyAlaPheLeuGly 370 	331 GlyGluPheThrCysH.sAlaArgH.sProLeuGlySerGlhHisValSerLeuSerLeu 350 	ProSerGlnProSerAspProclyValLeuGluLeuProArgValGlnValGluHisGlu	291 ValThrHisSerSerProProAlaArgLeuSerTrpThrGlnArgGlyGlnValLeuSer 310	AsnLeuGlyAsnGlyThrSerLeuProValLeuGluGlyGlnSerLeuCysLeuValCys	253ProProGluAsnLeuArgValMetValSerGlnAlaAsnArgThrValLeuGlu 270	2	52	252	712 CAGCCCCCTGCCACACTGAGCTGGGTCCTGCAGAACAGAGTCCTCTCCTCGTCCCATCCC 771	252 252	652 GTCCCATACCTGGAAGCCCAAAAAGGCCAGTTCCTGCGGCCTCCTCTGTGCTGCTGACAGC 711	252 252	241 LeuVallleSerIleSerArgAspAsnThrProAsp	221 ArgLysG1yValSerAlaGInArgThrValArgLeuArgValAlaTyrAlaProArgAsp 240 	201 SerPheThrProArgProGlnAspHisAspThrAspLeuThrCysHisValAspPheSer 220	181 ThrGlyAlaAlaLeuSerSerGlnGlyThrLysProThrThrSerHisPheSerValLeu 200	465 465	161 ThrValIleCysValPheAsnTrpAlaPheGluGluCysProProProSerPheSerTrp 180		406 GAGAGAGGAAGCTATGAGATATAATTTCATGAACGATGGGTTCTTTCT	21 GluArgGlySerTyrValArgTyrAsnPheMetAsnAspGlyPhePheLeuLysValThr	101 cysselledvallierigksphildelimetetinkspelbetetilijeritetiekigval 120 	86 GAGGTGGAAATGAGCACCCGGGGCCGATTCCAGCTCACTGGGGGATCCCCGCCAAGGGGAAC

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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acide Encoding the Same
FILE REFERENCE: P2630PIC17
CURRENT APPLICATION NUMBER: US/09/978,403A
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 60/062250
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US-09-978-403A-258
; Sequence 258, Application US/09978403A
; Sequence 100 No. US20030050240A1
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APPLICANT: Ashkenazi,
APPLICANT: Baker Kev:
APPLICANT: Botstein,
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TTCCAA 1677
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                     Paoni,
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                                                                                                                                                                                                                                                                                                                                                              Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                       James;
                                                                                                                                                                                                                                                                                                                                            Sophia S.
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                                                                                                                                                                                                                                                                                     Nicholas F.
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OR APPLICATION NUMBER: 60/079923
OR APPLICATION NUMBER: 60/080105
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
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OR APPLICATION NUMBER: 60/079656
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DR APPLICATION NUMBER: 60/081203
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PR APPLICATION NUMBER: 60/064249
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DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066364
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OR APPLICATION NUMBER: 60/083742
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OR FILING DATE: 1998-05-05
OR APPLICATION NUMBER: 60/084366
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OR APPLICATION NUMBER: 60/082804
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 ArgProArgProGluAl&ArgMetProLysGlyThrGlnAl&AspTyrAlaGluValLys
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US-09-978-564A-258
Sequence 258, App
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APPLICANT: Pan, James
APPLICANT: Pani, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C25
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: US/09/978,564A
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-03-11
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PRIOR APPLICATION NUMBER: 60/077791
PRIOR APPLICATION NUMBER: 60/07791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078086
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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Percent Similarity:
Best Local Similarity:
Query Match:
DB: Pred. No.: Score: 9.93e-221 2265.00 74.92% 74.75% 83.70% Length:
Matches:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C65
CURRENT APPLICATION NUMBER: US/09/999,833A
CURRENT FILLING DATE: 2001-10-24
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OR APPLICATION NUMBER: 60/06364
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RAPPLICATION NUMBER: 60/079294

REFILING DATE: 1998-03-25

OR APPLICATION NUMBER: 60/079656

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141 AlaLeuThrGlnLysProAspValTyrIleProGluThrLeuGluProGlyGlnProVal 16	121 GluargGlySerTyrValargTyrasnPheMetasnAspGlyPhePheLeuLysValThr 1 	1 CysSerLeuVallleArgAspAlaGlnMetGlnAspGluSerGlnTyrPhePheArgVal 	Qy 81 GluValGluMetSerThrArgGlyArgPheGlnLeuThrGlyAspProAlaLysGlyAsn 100	61 PheLysAlaValThrGluThrThrLysGlyAlaProValAlaThrAsnHisGlnSerArg 8 	41 CysSerPheSerTyrProArgGlnAspTrpThrGlySerThrProAlaTyrGlyTyrTrp 60 	Qy 21 PheTrpIleArgValGlnGluSerValMetValProGluGlyLeuCysIleSerValPro 40	1 Met.LeuLeuProLeuLeuLeuSerSerLeuLeuCluGly	: 83.70% Indels: Gaps: 11.2764	Similarity: 74.92% Sal Similarity: 74.75%	9.93e-221 Length:	Allgoment Scores.	PRIO	PRIO	PRIO	PRIO	PRIC	PRIOR FILING DATE: 1998-05-15 PRIOR FILING DATE: 1998-05-15 PRIOR FILING DATE: 1998-05-15	PRIO	PRIC	אלים מאלים מאלים	PRIC	PRIC	PRIC	PRIC	PRIC	PRIC
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Sear Job 1	Qy Db	Db Q	Оy	Оy	Ωу	ф
Search completed: October 8, 2003, 22:50:19 Job time : 477 secs	511 PheGln 512 1672 TTCCAA 1677	491 ArgProArgProGluAlaArgMetProLysGlyThrGlnAlaAspTyrAlaGluValLys 510 	471 ProGluSerGlnGluSerGlnGluGluLeuHisTyrAlaThrLeuAsnPheProGlyVa1 490 	451 AsnGlnLysLysGlnTyrGlnLeuProSerPheProGluProLysSerSerThrGlnAla 470 	431 ThrProAsnSerProArgThrProLeuProProGlyAlaProSerProGluSerLysLys 450	1372 GATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGCC 1431